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(54) Title: INTERCONVERSION OF PLANT FATTY ACID DESATURASES AND HYDROXYLASES			
(57) Abstract			
<p>A method is provided for modifying a fatty acyl desaturase to a fatty acyl hydroxylase consisting of identifying and changing as few as four amino acid residues that are conserved in functionally equivalent desaturase enzymes from various plant species but that are not identical in fatty acyl hydroxylases that exhibit significant overall sequence similarity to the fatty acyl desaturases, and which catalyze hydroxylation at one of the carbon residues on the fatty acyl substrate that is desaturated by the corresponding desaturase; the modifications being made by changing the amino acid residue so that it is identical or functionally equivalent to the amino acid residue found in the naturally occurring hydroxylase. Also provided is a similar method of modifying a fatty acyl hydroxylase to a fatty acyl desaturase by changing seven or fewer amino acid residues. Transgenic plants and products of such transgenic plants wherein the plants have been modified to produce a modified hydroxylase or desaturase are also provided.</p>			

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## INTERCONVERSION OF PLANT FATTY ACID DESATURASES AND HYDROXYLASES

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### FIELD OF THE INVENTION

The present invention concerns the modification of nucleic acid sequences and constructs, and methods related thereto, and the use of these sequences and constructs to produce modified enzymes which exhibit altered catalytic activities. The modified nucleic acids are of utility in producing genetically modified plants for the purpose of altering the fatty acid composition of plant oils, waxes, and other fatty acid-containing compounds. Particularly, the present invention concerns the modification of nucleic acids for the selective production of plant fatty acid desaturases and hydroxylases.

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### BACKGROUND OF THE INVENTION

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In addition to common plant fatty acids such as linoleic or linolenic acids, a number of plant species accumulate hydroxylated fatty acids. For example, castor (*Ricinus communis*) accumulates a seed oil which may contain more than 80% ricinoleic acid ( $\Delta$ -12-hydroxyoctadec-cis-9-enoic acid). This industrial fatty acid, used in the fabrication of lubricants and certain types of nylon, is also present in a number of other unrelated plant species. Biosynthesis of ricinoleic acid in castor has been studied in detail (van de Loo et al., 1995). By a single enzymatic step involving a membrane bound iron-containing enzyme, oleic acid is esterified to phosphatidylcholine. The reaction requires molecular oxygen, NAD(P)H and cytochrome b5 as an electron donor. In all these aspects, oleate hydroxylation has extensive similarity to microsomal oleate desaturation, a key step in the biosynthesis of linoleic acid. Genes encoding the castor and *Lesquerella fendleri* oleate hydroxylases have been identified and the gene products have been shown to have a high degree of sequence similarity to plant oleate desaturases (van de

Loo et al., 1995; Broun et al., 1997).

The castor oleate hydroxylase is about 70% identical to some oleate desaturases, and contains clusters of histidine residues diagnostic of class III diiron-oxo proteins, which include: plant desaturases FAD2, FAD3, FAD5, FAD6, FAD7, FAD8, bacterial alkane and xylene hydroxylases, carotene hydroxylase, carotene ketolase, and sterol methyl oxidases among others (Shanklin et al., 1997). The oleate hydroxylase from the crucifer *Lesquerella fendleri* shows about 81% sequence identity to the oleate desaturase from the crucifer *Arabidopsis thaliana* and about 71% sequence identity to the oleate hydroxylase from the more distantly related species, *Ricinus communis* (Broun et al., 1998). The observation that two different crucifer enzymes are more closely related than the two hydroxylases, and the presence of ricinoleic acid in a small number of distantly related plant species, suggests that the capacity to synthesize ricinoleate has arisen independently several times during the evolution of higher plants, by the genetic conversion of desaturases to hydroxylases.

All higher plants contain one or more oleate desaturases that catalyze the O<sub>2</sub>-dependent insertion of a double bond between carbons 12 and 13 of lipid-linked oleic acid (18:1<sup>n-9</sup>) to produce linoleic acid (18:2<sup>n-9,12</sup>) (Shanklin et al., 1998). By contrast, only fourteen species in ten plant families have been found to accumulate the structurally related hydroxy fatty acid, ricinoleic acid (D-12-hydroxyoctadec-cis-9-enoic acid) (van de Loo et al., 1993). Ricinoleic acid is synthesized by hydroxylation of oleic acid by enzymes that have similar enzymatic properties and exhibit a high degree of sequence similarity to oleate desaturases (Moreau et al., 1981 and van de Loo et al., 1995). The oleate desaturases and hydroxylases are integral membrane proteins, which are members of a large family of functionally diverse enzymes that includes alkane hydroxylase/alkene epoxidase, xylene monooxygenase, carotene ketolase, and sterol methyl oxidase (Shanklin et al., 1998). Biochemical evidence suggests that these nonheme iron-containing enzymes use a diiron-cluster for catalysis (Shanklin et al., 1997). They contain three equivalent histidine clusters that have been implicated in iron binding and shown to be essential for catalysis for several desaturases (Shanklin et al., 1998). This class of integral membrane proteins exhibit no significant sequence identity to the soluble diiron-containing enzymes which represent a similar diversity of enzymatic activities that include plant acyl-ACP desaturases, methane monooxygenase, propene monooxygenase and the R2 component of ribonucleotide reductase (Shanklin et al., 1998). From the results disclosed herein which demonstrate that amino acid substitution at certain conserved residues in the hydroxylase and desaturase enzymes confer enzymatic function, it is likely that plant oleate hydroxylase genes and desaturase genes are

evolutionarily related.

Most of the plant species that are grown for production of oils do not produce significant amounts of hydroxylated fatty acids. Thus, there is interest in being able to modify oil-producing species so that they produce hydroxylated fatty acids. This may be accomplished by the  
5 introduction of genes encoding fatty acyl hydroxylases. Plant genes for fatty acyl hydroxylases from *R. communis* and *L. fendleri* have been described and have been shown to be useful for modifying plants to produce hydroxylated fatty acids (Broun and Somerville, 1997). In addition, methods for using these genes to isolate hydroxylase genes from other plants have been described in U.S. Appln. Nos. 08/530,862 and 08/597,313; and international Appln. Nos. PCT/US95/11855  
10 (WO 96/10075) and PCT/US97/02187 (WO 97/30582), the complete disclosure of which is fully incorporated herein by reference.

In the aforementioned patent applications, we disclosed that an alternative method for the production of hydroxylated fatty acids is to modify a fatty acyl desaturase so that it catalyzes fatty acyl hydroxylation instead of, or in addition to, fatty acyl desaturation. Conversely, since it is also  
15 useful to control the degree of fatty acyl unsaturation in transgenic plants by the expression of introduced genes, it is also potentially useful to modify a fatty acyl hydroxylase so that it catalyzes fatty acyl desaturation. Such a modified gene could be used to increase the amount of desaturase activity in a plant.

In order to identify which amino acid residues are responsible for the different catalytic  
20 activities of the oleate hydroxylases and the oleate desaturases, the castor and *L. fendleri* oleate hydroxylase sequences are compared herein with the sequences of various oleate desaturases. The concept underlying this comparison was that if a particular residue was conserved in all known oleate desaturases but differed from the castor and *L. fendleri* oleate hydroxylases, it could be important in determining the outcome of the reaction. By contrast, if a particular residue was  
25 not conserved among the desaturases, it was unlikely to be responsible for the outcome of the reaction. The results of this comparison indicate that there are only seven amino acid residues which are conserved among all the desaturases but which differ in the oleate hydroxylases. These seven amino acid residues were disclosed in the aforementioned patent applications. Four of the seven critical residues are very close to putative iron ligands suggesting a role for these amino  
30 acids in protein function.

Once the amino acid residues of interest have been defined, there are many methods for producing genes encoding modified enzymes, including mutagenesis of existing genes and synthesis of novel genes. The most specific way of obtaining modified enzymes is by

site-directed mutagenesis, enabling specific substitution of one or more amino acids by any other desired amino acid. Site-directed mutagenesis can be performed, after cloning the encoding gene, by mutagenesis in vitro or in vivo and expression of the encoded enzyme by causing transcription and translation of the mutated gene in a suitable host cell.

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## SUMMARY OF THE INVENTION

In one aspect, the present invention provides novel modified hydroxylase and desaturase enzymes, obtained by expression of genes encoding said enzymes having amino acid sequences  
10 which differ in at least one amino acid from the corresponding wild-type enzymes. These mutant enzymes exhibit novel catalytic properties for modifying plant oil composition. A preferred embodiment of the invention is a mutant of the *Arabidopsis thaliana* FAD2 desaturase.

It is a one object of this invention to provide specific amino acid substitutions that result in the conversion of an enzyme which exhibits primarily oleate hydroxylase activity to an enzyme  
15 which exhibits more oleate desaturase activity than oleate hydroxylase activity. It is a further object of this invention to provide seven or fewer specific amino acid substitutions that result in the conversion of an enzyme which exhibits primarily oleate hydroxylase activity to an enzyme which exhibits more oleate desaturase activity than oleate hydroxylase activity.

It is also an object of this invention to provide specific amino acid substitutions that result  
20 in the conversion of an enzyme which exhibits primarily oleate desaturase activity to an enzyme which exhibits more oleate hydroxylase activity than oleate desaturase activity. It is a further object of this invention to provide as few as four specific amino acid substitutions that result in the conversion of an enzyme which exhibits primarily oleate desaturase activity to an enzyme which exhibits more oleate hydroxylase activity than oleate desaturase activity.

25 It is a further object of this invention to describe a general method by which any fatty acyl desaturase can be converted to a fatty acyl hydroxylase. It is a yet further object of this invention to disclose a general method by which any fatty acyl desaturase can be converted to a fatty acyl hydroxylase.

In another aspect, the invention provides a transgenic plant, comprising a plant that has  
30 been modified by the introduction of a gene for a modified hydroxylase.

It is a further object of the invention to provide a transgenic plant, comprising a plant that has been modified by the introduction of a gene for a modified desaturase.

In a further aspect this invention provides a system, which identifies and produces mutant

fatty acyl desaturase, hydroxylase, desaturase/hydroxylase enzymes with novel properties that can be used to modify plant oil composition.

These and other aspects of the invention will be further outlined in the detailed description hereinafter.

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## BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a multiple sequence alignment of deduced amino acid sequences for oleate hydroxylases and microsomal  $\Delta 12$  desaturases. Abbreviations are: Rcfah12, oleate 12-hydroxylase gene from *R. communis* (van de Loo et al., 1995); LFAH12, oleate 12-hydroxylase gene from *L. fendleri*; Atfad2, FAD2 desaturase from *Arabidopsis thaliana* (Okuley et al., 1994); Gmfad2-1, FAD2 desaturase from *Glycine max* (GenBank accession number L43920); Gmfad2-2, FAD2 desaturase from *Glycine max* (Genbank accession number L43921); Zmfad2, FAD2 desaturase from *Zea mays* (PCT/US93/09987).

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Figure 2 shows a general strategy for site-directed mutagenesis of *A. thaliana* FAD2 oleate desaturase.

Figure 3 shows the nucleic acid sequence of the coding region of the *A. thaliana* FAD2 oleate desaturase gene and the corresponding amino acid sequence of the enzyme.

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Figure 4 shows a general strategy for introducing seven mutations into the *A. thaliana* FAD2 gene.

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Figure 5 shows a comparison of the nucleic acid sequences of the coding regions of the *A. thaliana* FAD2 gene and the mFAD2 gene.

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Figure 6 shows a comparison of the deduced amino acid sequences of the *A. thaliana* FAD2 gene and mFAD2 gene.

Figure 7 shows a comparison of the nucleic acid sequences of the coding regions of the *L. fendleri* FAH12 gene and the mFAH12 gene.

Figure 8 shows a comparison of the deduced amino acid sequences of the *L. fendleri* FAH12 gene and the mFAH12 gene.

Figure 9 shows the fatty acid composition of yeast cells expressing desaturase and hydroxylase genes.

Figure 10 shows the genetic complementation of the Arabidopsis *fad2* mutation with the m<sub>7</sub>LFAH12 gene.

Figure 11 shows the fatty acid content of seed lipids from independent transgenic Arabidopsis lines expressing m<sub>7</sub>FAD2 or m<sub>4</sub>FAD2 under control of the *B. napus* napin promoter.

Figure 12 shows the contribution of individual amino-acid substitutions to the activity of the modified *Lesquerella* hydroxylase.

## DETAILED DESCRIPTION OF THE INVENTION

One subject of this invention is a class of enzymes, designated fatty acyl hydroxylases, that introduce a hydroxyl group into fatty acids. For example, the fatty acyl hydroxylases of the invention can catalyze hydroxylation of oleic acid to 12-hydroxy oleic acid (i.e., ricinoleic acid) and icosenoic acid to 14-hydroxy icosenoic acid (i.e., lesquerolic acid). This enzyme is referred to herein as "oleate hydroxylase". These enzymes have also been referred to as a class of kappa hydroxylases to indicate that the enzyme introduces the hydroxyl group three carbons distal (i.e., away from the carboxyl carbon of the acyl chain) from a double bond located near the center of the acyl chain.

A second subject of this invention is a class of enzymes, designated fatty acyl desaturases, that introduce double bonds into fatty acids. For example, fatty acyl desaturases of the invention can introduce a double bond between carbons 12 and 13 (counting from the carboxyl end) of eighteen carbon fatty acids. This enzyme is referred to herein as "oleate desaturase".

The above enzymes are named oleate hydroxylase and oleate desaturase in accordance with their discovery in oleate-containing plants. However, we have previously shown that the native enzymes are able to metabolize fatty acids with chain lengths other than eighteen carbons. Similarly, the present invention is not limited to metabolizing oleic acid but can also produce

saturated and/or hydroxylated fatty acids of varying chain lengths. Preferred are substrates with chain lengths of 16, 18, 20 and 22 carbons.

For example, the following fatty acids are also the subject of this invention: palmitoleic acid, hexadec-*cis*-9-enoic (16:1<sup>*cis*Δ<sup>9</sup></sup>); hydroxypalmitoleic acid, 12-hydroxy-hexadec-*cis*-9-enoic (12OH-16:1<sup>*cis*Δ<sup>9</sup></sup>); oleic acid, octadec-*cis*-9-enoic acid (18:1<sup>*cis*Δ<sup>9</sup></sup>); ricinoleic acid, 12-hydroxyoctadec-*cis*-9-enoic acid (12OH-18:1<sup>*cis*Δ<sup>9</sup></sup>); octadec-*cis*-9,15-dienoic acid (18:2<sup>*cis*Δ<sup>9,15</sup></sup>); densipolic acid, 12-hydroxyoctadec-*cis*-9,15-dienoic acid (12OH-18:2<sup>*cis*Δ<sup>9,15</sup></sup>); icosenoic acid (20:1<sup>*cis*Δ<sup>11</sup></sup>); lesquerolic acid, 14-hydroxy-*cis*-11-icosenoic acid (14OH-20:1<sup>*cis*Δ<sup>11</sup></sup>); *cis*-11,17-icosadienoic acid (14OH-20:2<sup>*cis*Δ<sup>11,17</sup></sup>); auricolic acid, 14-hydroxy-*cis*-11,17-icosadienoic acid (14OH-20:2<sup>*cis*Δ<sup>11,17</sup></sup>); erucic acid, docos-*cis*-13-enoic acid (22:1<sup>*cis*Δ<sup>13</sup></sup>); and hydroxyerucic acid, 16-hydroxydocos-*cis*-13-enoic acid (16OH-22:1<sup>*cis*Δ<sup>13</sup></sup>). It should be noted that icosenoic acid is sometimes spelled eicosenoic acid.

A further subject of this invention is the creation of modified genes encoding modified enzymes which have novel catalytic activities. The term "modified enzyme" as used herein always refers to the product of a modified gene rather than to any direct modification of the corresponding wild-type (WT) protein. Thus, we describe modified enzymes which before genetic modification had desaturase activity but did not exhibit detectable hydroxylase activity, but which after modification exhibit hydroxylase activity. We refer to these enzymes as "synthetic oleate hydroxylases". This designation does not preclude the possibility that the modified enzyme may also retain some amount of desaturase activity.

Similarly, we describe modified enzymes which before modification had oleate hydroxylase activity but had low levels of oleate desaturase activity relative to the amount of hydroxylase activity, but which after modification exhibit higher levels of oleate desaturase activity. We refer to these enzymes as "synthetic oleate desaturases". This designation does not preclude the possibility that the modified enzyme may also retain some amount of hydroxylase activity.

This invention is based on the discovery that plant oleate hydroxylases and oleate desaturases are structurally related enzymes (van de Loo et al., 1995). Indeed, because these enzymes are highly similar in primary structure, we have previously described methods for distinguishing between the two types of enzymes based on a comparison of the amino acid sequences (U.S. Appln. Nos. 08/530,862 and 08/597,313; international Appln. Nos. PCT/US95/11855 (WO 96/10075) and PCT/US97/02187 (WO 97/30582), referred to herein above. Based on the deduced amino acid sequences, we showed that the seven amino acid

residues that were completely conserved in all of the known oleate desaturases, were replaced by different amino acid residues in the only two oleate hydroxylase sequences known at that time.

An object of this invention is a method to convert an oleate hydroxylase to an oleate desaturase. We disclose that an oleate hydroxylase can be converted into an oleate desaturase by changing all seven conserved residues in oleate hydroxylases to the residues that would be found in oleate desaturases. We also show that the same effect can be accomplished by changing six residues. The observation that many combinations of six changes can convert a hydroxylase to a synthetic desaturase shows that no single amino acid change is absolutely required. Thus, there is no amino acid residue that is required for hydroxylase activity but not for desaturase activity.

10 This implies that the functionally significant difference between a hydroxylase and a desaturase is the conformation of the active site as comprised of the conserved amino acid residues. We conclude that changes in the conformation of the active site can change the outcome of the overall reaction.

One implication of this discovery is that any fatty acyl hydroxylase can be converted into a synthetic desaturase by making changes in the conformation of the active site. One aspect of this invention is a procedure for identifying the changes that are made to convert any hydroxylase to a desaturase.

An object of this invention is a method to convert an oleate desaturase into a synthetic oleate hydroxylase by changing all seven conserved residues in oleate desaturases to the residues that would be found in oleate hydroxylases. Based on the analysis of effects of mutations on the amount of desaturase activity exhibited by the LFAH12 hydroxylase, it appears clear that the functionally significant difference between a desaturase and a hydroxylase is the conformation of the active site.

Another implication of this discovery is that any desaturase can be converted into a hydroxylase by making changes in the conformation of the active site. One aspect of this invention is a procedure for identifying the relevant changes that need to be made to convert any desaturase to a synthetic hydroxylase. Changing of a subset of the seven amino acids, as few as four amino acids, results in the conversion of a desaturase to a synthetic hydroxylase. Similarly, changing of the seven, or fewer, amino acids can confer hydroxylase activity on a desaturase.

Thus, these seven amino acid positions define the active site of these fatty acyl enzymes.

30 Besides the genetic techniques exemplified herein, crystallographic and/or spectroscopic techniques may also be used to correlate changes in the active site with enzymatic function. Assays based on determining the chemical and physical properties of the enzymes may be

performed with substrate and/or cofactor analogs to slow or to stabilize the enzymatic reaction. This active site and its function is distinct from the histidine residues previously identified.

The description below applies equally to converting the enzymatic activity from hydroxylase to desaturase, as from desaturase to hydroxylase. In this respect, it should be understood that the functional consequences of modifying a fatty acyl metabolic enzyme (e.g., by genetic engineering) may be assayed by assaying the effects of the modified enzyme on plant fatty acid compounds, especially in seed oil. A modification of the fatty acyl metabolic enzyme may be determined to increase, decrease or not affect any enzymatic activity (e.g., desaturase, hydroxylase) by assaying the fatty acyl content of a cell or plant containing the modified enzyme.

10 A statistically significant increase or decrease in particular desaturated or hydroxylated fatty acids will identify modifications that increase or decrease, respectively, enzymatic activity.

Sequence comparison at the level of amino acid sequence, as well as the functional assays described herein, would show that the number of known nucleotide and amino sequences which are exemplified for fatty desaturases and hydroxylases may be expanded by computer analysis of information found in databases or gathered during sequencing projects to identify related sequences encoding desaturases and hydroxylases. Typically, amino acid sequences are considered to be related with as little as 70% or 80% similarity between the two polypeptides; however, at least 90% or 95% similarity is preferred; and at least 98% similarity is more preferred. Conservative amino acid substitutions may be considered when making sequence comparisons. See generally, Doolittle, *Of URFS and ORFS*, University Science Books, 1986; Gribskov and Devereux, *Sequence Analysis Primer*, Stockton Press, 1991; and references cited therein for algorithms known in the art and used in commercially available software for sequence analysis. A specific example of an algorithm that may be used to calculate sequence divergence is the nucleotide or amino acid versions of the BLAST computer program described by Altschul et al. (J. Mol. Biol., 215, 403-410, 1990; Proc. Natl. Acad. Sci. USA, 87, 5509-5513, 1990; Nucl. Acids Res., 25, 3389-3402, 1997), the complete disclosure of which is fully incorporated herein by reference.

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The method according to the present invention is suitable for the production, screening and selection of modified hydroxylase and desaturase enzymes which are derived from naturally existing enzymes. Such mutants are, for example, those encoded by a gene derived from a wild-type FAD2 gene of *A. thaliana* which can be converted to a synthetic oleate hydroxylase. The method can further be advantageously used for the selection of synthetic hydroxylases derived from desaturases other than FAD2-like desaturases. For example, we envision that any

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fatty acyl desaturase that shows amino acid sequence similarity to the *A. thaliana* FAD2 gene can be modified according to the teachings of this invention. In particular, it is readily possible to describe the changes necessary to convert the oleate desaturases from soybean, *Zea mays*, or castor to synthetic hydroxylases because the sequences of these enzymes can readily be aligned with the *A. thaliana* FAD2 gene product so that the conserved amino acid residues are aligned (Figure 1). Although the exact numbering of the relevant amino acid residues may change, the intention may be understood by reference to the example in which the numbering of the residues of the LFAH12 and FAD2 gene are aligned. In the LFAH12 gene, positions for substitution of particular interest include 63, 105, 149, 218, 296, 323, 325. The corresponding numbers based on the FAD2 sequence are 63, 104, 148, 217, 295, 322, 324. More generally, we envision that by comparison of the sequences of delta-9 stearyl-ACP desaturases and stearyl-9-hydroxylases it will be possible to identify the amino acid residues that are conserved in all delta-9 stearyl-ACP desaturases but which differ between delta-9 desaturases and 9-hydroxylases. Once such differences have been identified, the knowledge and methods taught herein can be used to create synthetic stearyl-9-hydroxylases. We also envision that it will be possible to create synthetic hydroxylases for which naturally occurring enzymes are not available.

In addition, a report by Lee et al. (1997) describes the isolation of a cDNA encoding an acetylenase from *Crepis alpina*. This cDNA is highly similar to plant delta-12-desaturase and the methods used to interconvert the desaturase and hydroxylase functionality may also teach how to interconvert desaturase and acetylenase and vice versa. Additionally, the *Pseudomonas oleovorans* alkane  $\omega$ -hydroxylase is equally efficient as an epoxidase when presented with 1-octene. Thus the genes encoding fatty acid 12-epoxidases, will also be found in species such as *Euphorbia lagascae* and *Stokesia laevis* that will be closely related to delta-12-desaturase. We envision that these enzymes will be active on linoleate rather than oleate, and will introduce a 12,13 epoxy group. Other lipid enzymes that modify the 12-position such as a ketolase may be related in a similar way as the desaturase and hydroxylase. The methods taught here will also teach how to interconvert any combination of these functionalities.

It will be clear that either oligonucleotide-aided site-directed mutagenesis or region-directed random mutagenesis can be used or any other suitable method for efficiently generating mutations in the hydroxylase or desaturase genes, including complete or partial synthesis of the gene. The method for selecting modified enzymes according to the present invention (which may also include identification, screening, and production) may comprises the following steps: mutagenizing a cloned gene encoding an enzyme of interest or a fragment thereof; isolating the

obtained mutant gene or genes; introducing said mutant gene or genes, preferably on a suitable vector, into a suitable host strain for expression and production; recovering the produced modified enzyme; and identifying those genes encoding modified enzymes having improved properties for application in modifying plant lipid composition. Although the specific examples presented here  
5 by way of illustration utilize site-directed mutagenesis, it will be obvious to those skilled in the art that other methods could be used to identify changes that serve equally well for the conversion of a desaturase to a synthetic hydroxylase, or vice versa. Similarly, it will be obvious to those skilled in the art that modified enzymes could also be produced by partial or complete synthesis of modified genes using currently available methods for oligonucleotide synthesis and composition  
10 of genes from oligonucleotides and/or fragments from preexisting genes.

Suitable host strains (e.g., bacteria, fungi, yeast, animal cells) for production of enzymes include transformable microorganisms in which expression of the enzymes can be achieved. Specifically, strains of *Saccharomyces cerevisiae* are among the preferred hosts. Expression of fatty acyl enzymes is obtained by using expression signals that function in the selected host  
15 organism. Expression signals include sequences of DNA regulating transcription and translation of the fatty acyl metabolizing genes. Proper vectors are able to replicate at sufficiently high copy numbers in the host strain of choice or enable stable maintenance of the introduced gene in the host strain by chromosomal integration.

Assays known in the art may be used to determine and quantify the activity of the  
20 modified enzymes in the microbial host. Results provided in the examples show that such results are useful predictors of the activity of the modified enzymes in transgenic plants. The properties of the naturally occurring or mutated enzymes may be enhanced by introducing a variety of mutations in the enzyme. For the most part, the mutations will be substitutions, either conservative or non-conservative, but deletions and insertions may also find use. Another aspect  
25 of the invention is the development of novel assays and other processes using the modified enzymes.

For conservative substitutions of "functionally equivalent amino acid residues" the following may be employed for guidance:

30 Aliphatic neutral non-polar G, A, P, L, I, V  
Aliphatic neutral polar C, M, S, T, N, Q  
Charged anionic D, E  
Cationic K, R

Aromatic F, H, W, Y

where any amino acid may be substituted with any other amino acid in the same chemical category, particularly on the same line. In addition, the polar amino acids N, Q may substitute or  
 5 be substituted for by the charged amino acids.

The following numbering is based on the *A. thaliana* FAD2 desaturase or, where indicated, the *Lesquerella* hydroxylase sequence, but the considerations are relevant to other desaturases and hydroxylases having a substantially homologous structure, particularly those having greater than about 70% to 98% similarity. Positions for substitution of particular interest  
 10 include 63, 105, 149, 218, 296, 323, 325 (numbering based on the LFAH12 sequence). The corresponding positions based on the FAD2 sequence are 63, 104, 148, 217, 295, 322, 324. At some positions there will be an intent to change an amino acid, while maintaining the general conformation and volume of the amino acid at that site.

15 Substitutions of particular interest include:

	63	V or A
	105	G or A
	149	N or T
20	218	F or Y
	296	V or A
	323	A or S
	325	I or M

25 Finally, it will be clear that by deletions or insertions of the amino acids in the desaturase or hydroxylase polypeptide chains, either created artificially by mutagenesis or naturally occurring in desaturases or hydroxylases similar to those described herein, the numbering of the amino acids may change. However, it is to be understood that positions corresponding to amino acid positions of the enzymes described herein will fall under the scope of the claims.

30

#### Genetic Engineering Applications:

As is well known in the art, the description herein of novel genes encoding plant enzymes that metabolizes fatty acids (i.e., desaturase, hydroxylase, or both activities) allows production of

nucleic acids (e.g., recombinant clones, expression constructs) that could be single- or double-stranded, and comprised of DNA, RNA, modified bases and nucleotides, or combinations thereof. Such polynucleotides may be genomic DNA, cDNA, cRNA, mRNA or heterogeneous RNA (hnRNA). The nucleic acid may contain introns; promoters, enhancers, silencers, transcription initiation/termination sites or other transcriptional regulatory regions; translation initiation/termination sites or other translational regulatory regions; translocation or cellular localization signals; transmembrane regions; regions that regulate message stability; polyadenylation sites; or combinations thereof. For example, a recombinant clone made by genetic engineering may be used to transfect plants, other organisms (e.g., bacteria, fungi, yeast), or cells thereof.

The nucleotide sequences which encode a plant fatty acyl enzyme (e.g., desaturase, hydroxylase, modified versions thereof) may be used in various constructs, for example, as probes to obtain further nucleic acids from the same or other species. Alternatively, these sequences may be used in conjunction with appropriate regulatory sequences to increase levels of the respective fatty acyl enzyme of interest in a host cell for the production of fatty acids with varying amounts of saturation/hydroxylation or study of the enzyme *in vitro* or *in vivo*, or to decrease or increase levels of the respective fatty acyl enzyme of interest for some applications when the host cell is a plant entity, including plant cells, plant parts (including, but not limited to, seeds, cuttings, and tissues), and plants.

A nucleotide sequence encoding a plant fatty acyl enzyme of the present invention may include genomic, cDNA or mRNA derived sequences. By "encoding" is meant that the sequence corresponds to a particular amino acid sequence either in a sense or anti-sense orientation. By "recombinant" is meant that the sequence contains a genetically engineered modification through manipulation via mutagenesis, nucleic acid modifying enzymes, or the like. A cDNA sequence may or may not encode pre-processing sequences, such as transit or signal peptide sequences. Transit or signal peptide sequences facilitate the delivery of the protein to a given organelle and are frequently cleaved from the polypeptide upon entry into the organelle, releasing the "mature" sequence. The use of the precursor DNA sequence is preferred in plant cell expression cassettes.

Furthermore, as discussed above, the complete genomic sequence of a wild-type plant fatty acyl enzyme may be obtained by the screening of a genomic library with a probe, such as a cDNA probe, and isolating those sequences which regulate expression in seed tissue. In this manner, the transcription and translation initiation regions, enhancers, silencers, introns, and/or transcript and translation termination regions of the plant fatty acyl enzyme may be obtained for

use in a variety of nucleic acid constructs, with or without the fatty acyl enzyme structural gene. Thus, nucleotide sequences corresponding to the plant fatty acyl enzyme of the present invention may also provide signal sequences useful to direct transport into an organelle, 5' upstream non-coding regulatory regions (promoters) having useful tissue and timing profiles, 3' downstream non-coding regulatory region useful as transcriptional and/or translational regulatory regions, or  
5 may lend insight into other features of the gene.

Once the desired plant fatty acyl enzyme nucleotide sequence is obtained, it may be manipulated in a variety of ways. Where the sequence involves non-coding flanking regions, the flanking regions may be subjected to resection, mutagenesis, etc. Thus, transitions, transversions, deletions, and insertions may be performed on the naturally occurring sequence. In addition, all or  
10 part of the sequence may be synthesized. In the structural gene, one or more codons may be modified to provide for a modified amino acid sequence, or one or more codon mutations may be introduced to provide for a convenient restriction site, or other purposes involved with construction or expression. The structural gene may be further modified by employing synthetic  
15 adapters, linkers to introduce one or more convenient restriction sites, or the like.

The nucleotide or amino acid sequences encoding a plant fatty acyl enzyme of the present invention may be combined with other non-native, or "heterologous", sequences in a variety of ways. By "heterologous" sequences is meant any sequence which is not naturally found joined to the plant fatty acyl enzyme, including, for example, combination of nucleotide sequences from the  
20 same plant which are not naturally found joined together. Analogously, a "heterologous" nucleic acid describes nucleic acid which is introduced into a host cell or organism which does not naturally contain the nucleic acid.

Using the nucleotide and amino acid sequences disclosed herein, compositions of the present invention may be made substantially pure by overexpressing the nucleic acid or peptide  
25 and isolating same. By "substantially pure", a composition of a molecule is described as being at least 80%, preferably at least 90%, more preferably at least 95%, and most preferably at least 99% pure by weight as compared to other substances (i.e., contaminants) of the same chemical character as the recited molecule (e.g., lipid, nucleic acid, protein).

The DNA sequence encoding a plant fatty acyl enzyme of the present invention may be  
30 employed in conjunction with all or part of the gene sequences normally associated with the fatty acyl enzyme. In its component parts, a DNA sequence encoding fatty acyl enzyme is combined in a DNA construct having, in the 5' to 3' direction of transcription, a transcription initiation control region capable of promoting transcription and translation in a host cell, the DNA sequence

encoding plant fatty acyl enzyme, and transcription and translation termination regions.

Potential host cells include both prokaryotic and eukaryotic cells. A host cell may be unicellular or found in a multicellular differentiated or undifferentiated organism depending upon the intended use. Cells of the present invention may be distinguished by having a plant fatty acyl enzyme foreign to the wild-type cell present therein, for example, by having a recombinant nucleic acid construct encoding a plant fatty acyl enzyme therein.

Depending upon the host, the regulatory regions will vary, including regions from viral, plasmid or chromosomal genes, or the like. For expression in prokaryotic or eukaryotic microorganisms, particularly unicellular hosts, a wide variety of constitutive or regulatable promoters as well as terminators may be employed. Expression in a microorganism can provide a ready source of the plant enzyme. Among transcriptional initiation regions which have been described are regions from bacterial and fungal (e.g., mold, yeast) hosts, such as *E. coli*, *B. subtilis*, *Saccharomyces cerevisiae*, including promoters such as lacUV5 or a derivative such as trc; bacteriophage T3, T7 or SP6 promoters; trpE; ADC1, Gal1, Gal10, PHO5, or the like.

For the most part, the constructs will involve regulatory regions functional in plants which provide for modified production of plant fatty acyl enzyme with resulting modification of the fatty acid composition. The open reading frame, coding for the plant fatty acyl enzyme or functional fragment thereof will be joined at its 5' end to a transcription initiation regulatory region such as the wild-type sequence naturally found 5' upstream to the fatty acyl enzyme structural gene. Numerous other transcription initiation regions are available which provide for a wide variety of constitutive or regulatable (e.g., inducible) transcription of the structural gene. Among transcriptional initiation regions used for plants are such regions associated with the structural genes such as for nopaline and mannopine synthases, or with napin, soybean  $\beta$ -conglycinin, oleosin, 12S storage protein, the cauliflower mosaic virus 35S promoters, or the like. The transcription/ translation initiation regions corresponding to such structural genes are found immediately 5' upstream to the respective start codons. In embodiments wherein the expression of the fatty acyl metabolic protein is desired in a plant host, the use of all or part of the complete plant fatty acyl enzyme gene is desired, namely all or part of the 5' upstream non-coding regions (promoter) together with the structural gene sequence and 3' downstream non-coding regions may be employed. If a different promoter is desired, such as a promoter native to the plant host of interest or a modified promoter, i.e., having transcription initiation regions derived from one gene source and translation initiation regions derived from a different gene source, including the sequence encoding the plant fatty acyl enzyme of interest, or enhanced promoters, such as double

35S CaMV promoters, the sequences may be joined together using standard techniques.

For such applications when 5' upstream non-coding regions are obtained from other genes regulated during seed maturation, those preferentially expressed in plant embryo tissue, such as transcription initiation control regions from the *B. napus* napin gene, or the *Arabidopsis* 12S storage protein, or soybean  $\beta$ -conglycinin (Bray et al., 1987), or the plant fatty acyl hydroxylase promoter are desired. Transcription initiation regions which are preferentially expressed in seed tissue, i.e., which are undetectable in other plant parts, are considered desirable for fatty acid modifications in order to minimize any disruptive or adverse effects of the gene product.

Regulatory transcription termination regions may be provided in DNA constructs of the present invention as well. Transcription termination regions may be provided by the DNA sequence encoding the plant fatty acyl enzyme or a convenient transcription termination region derived from a different gene source, for example, the transcription termination region which is naturally associated with the transcription initiation region. Where the transcription termination region is from a different gene source, it will contain at least about 0.5 kb, preferably about 1-3 kb of sequence 3' to the structural gene from which the termination region is derived.

Plant expression or transcription constructs having a plant fatty acyl enzyme as the DNA sequence of interest for increased or decreased expression thereof may be employed with a wide variety of plant life, particularly, plant life involved in the production of vegetable oils. Most especially preferred are temperate oilseed crops. Plants of interest include, but are not limited to rapeseed (canola and high erucic acid varieties), *Crambe*, *Brassica juncea*, *Brassica nigra*, meadowfoam, flax, sunflower, safflower, cotton, *Cuphea*, soybean, peanut, coconut and oil palms and corn. An important criterion in the selection of suitable plants for the introduction of the fatty acyl enzyme is the presence in the host plant of a suitable substrate for the fatty acyl enzyme. Thus, for example, production of vernolic acid will be best accomplished in plants that normally have high levels of linoleic acid in seed lipids.

Depending on the method for introducing the recombinant constructs into the host cell, other DNA sequences may be required. Importantly, the present invention is applicable to dicotyledons and monocotyledons species alike and will be readily applicable to new and/or improved transformation and regulation techniques. The method of transformation is not critical to the present invention: various methods of plant transformation are currently available. As newer methods are available to transform crops, they may be directly applied hereunder. For example, many plant species naturally susceptible to *Agrobacterium* infection may be successfully transformed via tripartite or binary vector methods of *Agrobacterium* mediated transformation. In

addition, techniques of microinjection, particle bombardment, and electroporation have been developed which allow for the transformation of various monocot and dicot plant species.

In developing the DNA construct, the various components of the construct or fragments thereof will normally be inserted into a convenient cloning vector which is capable of replication in a bacterial host, e.g., *E. coli*. Numerous vectors exist that have been described in the literature (e.g., plasmid, bacteriophage, cosmid, yeast artificial chromosome or YAC, bacterial artificial chromosome or BAC). After each cloning, the plasmid may be isolated and subjected to further manipulation, such as restriction, insertion of new fragments, ligation, deletion, insertion, resection, etc., so as to tailor the components of the desired sequence. Once the construct has been completed, it may then be transferred to an appropriate vector for further manipulation in accordance with the manner of transformation of the host cell.

Normally, included with the DNA construct will be a structural gene having the necessary regulatory regions for expression in a host and providing for selection of transformant cells. The gene may provide for resistance to a cytotoxic agent, e.g., antibiotic, heavy metal, toxin, etc., complementation providing prototrophy to an auxotrophic host, viral immunity, or the like. Depending upon the number of different host species the expression construct or components thereof are introduced, one or more markers may be employed, where different conditions for selection are used for the different hosts.

It is noted that the degeneracy of the DNA code provides that codon substitutions are permissible in the nucleotide sequence contained in nucleic acids of the present invention without any corresponding modification of the amino acid sequence.

As mentioned above, the manner in which the DNA construct is introduced into the plant host is not critical to the present invention. Any method which provides for efficient transformation may be employed. Various methods for plant cell transformation include the use of Ti- or Ri-plasmids, microinjection, electroporation, infiltration, imbibition, DNA particle bombardment, liposome fusion, DNA bombardment, or the like. In many instances, it will be desirable to have the DNA construct bordered on one or both sides of the T-DNA, particularly having the left and right borders, more particularly the right border. This is particularly useful when the construct uses *A. tumefaciens* or *A. rhizogenes* as a mode for transformation, although the T-DNA borders may find use with other modes of transformation.

Where *Agrobacterium* is used for plant cell transformation, a vector may be used which may be introduced into the *Agrobacterium* host for homologous recombination with T-DNA or the Ti- or Ri-plasmid present in the *Agrobacterium* host. The Ti- or Ri-plasmid containing the T-

DNA for recombination may be armed (capable of causing gall formation) or disarmed (incapable of causing gall), the latter being permissible, so long as the *vir* genes are present in the transformed *Agrobacterium* host. The armed plasmid can give a mixture of normal plant cells and gall.

5 In some instances where *Agrobacterium* is used as the vehicle for transforming plant cells, the expression construct bordered by the T-DNA border(s) will be inserted into a broad host spectrum vector, there being broad host spectrum vectors described in the literature. Commonly used is pRK2 or derivatives thereof. See, for example, Ditta et al. (1980). Included with the expression construct and the T-DNA will be one or more markers, which allow for selection of  
10 transformed *Agrobacterium* and transformed plant cells. A number of markers have been developed for use with plant cells, such as resistance to kanamycin, the aminoglycoside G418, hygromycin, or the like. The particular marker employed is not essential to the present invention, one or another marker being preferred depending on the particular host and the manner of construction.

15 For transformation of plant cells using *Agrobacterium*, explants may be combined and incubated with the transformed *Agrobacterium* for sufficient time for transformation, the bacteria killed, and the plant cells cultured in an appropriate selective medium. Once callus forms, shoot formation can be encouraged by employing the appropriate plant hormones in accordance with known methods and the shoots transferred to rooting medium for regeneration of plants. The  
20 plants may then be grown to seed and the seed used to establish repetitive generations and for isolation of vegetable oils.

Polypeptides with fatty acyl enzymatic activity may be isolated using the identified nucleic acid sequence. The polypeptide may be isolated from natural sources (i.e., plants) or from host cells expressing recombinant fatty acyl enzyme sequences. Polypeptides may be purified using  
25 centrifugation, precipitation, specific binding, electrophoresis, and/or chromatography. Separation may be facilitated using enzyme substrates, antibody and/or attachment of a fusion peptide (e.g., avidin, glutathione S-transferase, poly-His, maltose binding protein, myc 9E10-epitope, protein A/G, SV40 T antigen).

Detection of protein expression and localization is facilitated by fusions with reporters  
30 such as, for example, alkaline phosphatase (AP),  $\beta$ -galactosidase (LacZ), chloramphenicol acetyltransferase (CAT),  $\beta$ -glucuronidase (GUS), green fluorescent protein (GFP),  $\beta$ -lactamase, luciferase (LUC), or derivatives thereof. Such reporters would use cognate substrates that are preferably assayed by a chromogen, fluorescent, or luminescent signal.

Transcriptional and/or translational fusions of the fatty acyl gene or enzyme and a heterologous nucleic acid or peptide, respectively, may be made. In a transcriptional fusion, a non-translated region of the heterologous gene may be ligated to the fatty acyl metabolic gene or, alternatively, a non-translated region of the fatty acyl gene may be ligated to the heterologous gene. The reading frames of the peptide which is a fatty acyl enzyme and a heterologous peptide may be joined in a translational fusion. If a reporter or selectable marker is used as the heterologous nucleic acid/peptide, then the effect of mutating the nucleotide/amino acid sequences of the fatty acyl enzyme or heterologous nucleic acid/peptide on fatty acid metabolism may be readily assayed. In particular, a transcriptional fusion may be used to localize a regulated promoter of the fatty acyl metabolic gene and a translational fusion may be used to localize the fatty acyl metabolic protein in the cell. For peptide fusions, a peptide recognition site for a protease (e.g., enterokinase, Factor Xa, thrombin) may be included.

#### Examples.

15

The following examples which detail materials and methods which can be employed in the practice of the principles of the present invention are offered by way of illustration and not by way of limitation.

#### 20 Oligonucleotides:

The oligonucleotides used for producing modified forms of the FAD2 gene and the Lfah12 gene are shown in Table 1.

Table 1. Oligonucleotides used for site directed mutagenesis. Letters in uppercase are homologous to the wild type FAD2 or LFAH12 sequences, mutations are in lower case. The mutations made by each oligonucleotide are shown by standard one-letter amino acid abbreviations (e.g., V63A is a mutation that replaces a valine residue at position 63 for an alanine residue).

5

	Name	Use	Amino-acid substitution	Primer sequence (*)
10	mH1f	a	V63A	ATCACTTTAG <u>c</u> TTCTTGCTTCT
	mH1r	a	V63A	AGAAGCAAGAA <u>g</u> CTAAAGTGAT
	mH2f	a	G105A	CTGGGTCATT <u>Gc</u> CCATGAATGTGGTCACC
	mH2r	a	G105A	GGTGACCACATTCATGG <u>g</u> CAATGACCCAG
	mH3f	a	N149T	CACCATTCCAACA <u>c</u> TGGATCCCTAGAA
15	mH3r	a	N149T	TTCTAGGGATCCA <u>g</u> TGTTGGAATGGTG
	mH4f	a	F218Y	CATGCACCTATCT <u>a</u> TAAGGACCGTG
	mH4r	a	F218Y	CACGGTCCTTA <u>a</u> AGATAGGTGCATG
	mH5f	a	V296A	AGAGGAGCTTTGG <u>c</u> TACGGTAGAC
	mH5r	a	V296A	GTCTACCGT <u>a</u> CCAAAGCTCCTCT
20	mH6f	a	A323S	CATCTCTTT <u>i</u> CAACTATACCGCATT
	mH6r	a	A323S	AATGCGGTATAGTT <u>Ga</u> AAAGAGATG
	mH7F	a	I325m	CATCTCTTTGCAACTAT <u>g</u> CCGCATT
	mH7r	a	I325M	AATGCGG <u>c</u> ATAGTTGCAAAGAGATG
	mH67f	a	A323S; I325M	CATCTCTTT <u>i</u> CAACTAT <u>g</u> CCGCATT
25	mH67r	a	A323S; I325M	AATGCGG <u>c</u> ATAGTT <u>Ga</u> AAAGAGATG
	H1f	b	A63V	ATCACTTTAG <u>t</u> TTCTTGCTTCT
	H1r	b	A63V	AGAAGCAAGAA <u>a</u> CTAAAGTGAT
30	H2f	b	A105G	CTGGGTCATT <u>Gg</u> CCATGAATGTGGTCACC
	H2r	b	A105G	GGTGACCACATTCATGG <u>c</u> CAATGACCCAG
	H3f	b	T149N	CACCATTCCAACA <u>a</u> TGGATCCCTAGAA
	H3r	b	T149N	TTCTAGGGATCCA <u>t</u> TGTTGGAATGGTG
	H4f	b	Y218F	CATGCACCTATCT <u>t</u> TAAGGACCGTG

Table 1. (continued)

	Name	Use	Amino-acid substitution	Primer sequence (*)
5	H4r	b	Y218F	CACGGTCCTT <u>Aa</u> AGATAGGTGCATG
	H5f	b	A296V	AGAGGAGCTTTGG <u>t</u> TACGGTAGAC
	H5r	b	A296V	GTCTACCGT <u>Aa</u> CCAAAGCTCCTCT
	H6f	b	S323A	CATCTCTTT <u>g</u> CAACTATACCGCATT
10	H6r	b	S323A	AATGCGGTATAGTT <u>Gc</u> AAAGAGATG
	H7f	b	M325I	CATCTCTTTGCAACTAT <u>a</u> CCGCATT
	H7r	b	M325I	AATGCGG <u>t</u> ATAGTTGCAAAGAGATG
	mD1f	c	A63V	GACATCATTATAG <u>t</u> CTCATGCTTCTACT
	mD1r	c	A63V	AGTAGAAGCATGAG <u>a</u> CTATAATGATGTC
15	mD2f	c	A104G	CTGGGTCATAG <u>g</u> CCACGAATGCGGTC
	mD2r	c	A104G	GACCGCATTCGTGG <u>c</u> CTATGACCCAG
	mD3f	c	T148N	CACCATTCCAACA <u>a</u> TGGATCCCTCGAA
	mD3r	c	T148N	TTCGAGGGATCC <u>a</u> tTGTTGGAATGGTG
	mD4f	c	Y217F	CCCCAACGCTCCCATCT <u>t</u> CAATGACCGAGA
20	mD4r	c	Y217F	TCTCGGTCATTG <u>a</u> AGATGGGAGCGTTGGGG
	mD5f	c	A295V	CAGGGGAGCTTTGG <u>t</u> TACCGTAGACAGAG
	mD5r	c	A295V	CTCTGTCTACGGT <u>Aa</u> CCAAAGCTCCCCTG
	mD67f	c	S322A; M324I	CACCTGTTC <u>g</u> CGACA <u>A</u> TaCCGCATTATAACGC
25	mD67r	c	S322A; M324I	GCGTTATAATGCGG <u>t</u> ATTGT <u>Cg</u> cGAACAGGTG
	H5'	(**)	d	(1) TATCGAaggcctGATGGGTGCT
	H3'	(**)	d	(2) CTCGCAGTATCgagctCATAACTTATTGTT
	D5'	(**)	d	(3) gatcggtacccgggATGGGTGCAGGTGGAAG- AATGCCGG
30	D3'	(**)	d	4 gatcgaattcgagctcTCATAACTTATTGTTGTA- CCAGTACACACC

(\*) Underlined: target codons for mutagenesis; lower-case letters in bold: oligonucleotide

35 mismatches with the target sequence for the introduction of the described amino-acid substitutions

(\*\*) Lower-case letters in bold: oligonucleotide mismatches with the target sequence for the introduction of restriction sites

(1) Oligonucleotide H5' adds a *Stu*I site immediately before LFAH12 initiating codon.

(2) Oligonucleotide H3' introduces a *Sac*I site following the terminator codon of LFAH12.

5 (3) Oligonucleotide D5' adds *Kpn*I and *Sma*I sites immediately before FAD2 initiating codon.

(4) Oligonucleotide D3' introduces restriction sites *Sac*I, *Eco*RV, and *Eco*RI sites following the terminator codon of FAD2.

The various uses were (a) introduction of all seven mutations into LFAH12, (b) to revert each of the seven mutations of m7FAH12 to their equivalents in the wt LFAH12 sequence in  
10 order to create all combinations of six of the seven changes of m7FAH12, (c) introduction of all seven mutations into FAD2, and (d) introduction of convenient restriction sites in the coding region of genes to facilitate subsequent cloning.

#### Plasmid Constructions:

15 The basic construct which was used to create modified hydroxylases from the *A. thaliana* FAD2 desaturase was named pYES-F2. This plasmid was constructed as follows. *A. thaliana* cDNA clone 146M12T7 encoding FAD2 was obtained from the Arabidopsis Stock Center at the Ohio State University. This cDNA sequence was amplified using *Pfu* DNA polymerase (Stratagene) in conjunction with primers designated D5' and D3' to introduce the flanking  
20 restriction sites, *Kpn*I and *Sma*I immediately preceding the initiation codon ATG, and *Sac*I and *Eco*RI restriction sites following the terminator codon TGA (Figure 2).

Restriction sites in oligonucleotide D5':

25 5' gatcggataccg<sup>g</sup>gATGGGTGCAGGTGGAAGAATGCCGG 3'  
                  ^      ^  
                  *Kpn*I *Sma*I

Restriction sites in oligonucleotide D3':

30 5' gatcgaattcgagctcTCATACTTATTGTTGTACCAGTACACACC 3'  
                  ^      ^  
                  *Eco*RI *Sac*I

This amplified wild type FAD2 fragment was cloned into the *EcoRV* site in the vector pZerO (Invitrogen). Following cloning into this high copy bacterial vector, both the coding and noncoding strands of the entire FAD2 insert were sequenced to confirm the presence of the expected sequence and to confirm the absence of secondary mutations that can arise from PCR amplification.

The insert was then excised by restriction with *KpnI* and *EcoRI* and cloned into the corresponding sites in the bacterial-yeast shuttle vector pYESII (Invitrogen). The pYESII-F2 plasmid was transformed into yeast strain INVSC2 (Invitrogen) by electroporation using a BTX electroporator (BTX).

Plasmid pBNL was used to produce transgenic plants containing the wild type FAD2 gene or modified versions of the gene. This plasmid was constructed as follows. The FAD2 insert in pYES-F2 was excised using the restriction enzymes *SmaI* and *SacI*. This fragment was cloned into a bacteria-plant shuttle vector pDN, behind the seed specific napin promotor using corresponding restriction sites to produce plasmid pBNL. This construct was introduced into *Agrobacterium tumefaciens* strain GV3101 pMP90 using electroporation (BTX). The agrobacterium was used to transform the FAD2 mutant of *A. thaliana* by vacuum infiltration (Bechtold et al., 1993), and transformants selected for by challenging seeds to germinate on kanamycin containing agarose.

#### Site-directed Mutagenesis:

Oligonucleotide PCR primers were designed to introduce nucleotide substitutions into LFAH12 and FAD2 through overlap-extension PCR (Ho et al., 1989). These included complementary oligonucleotides 22-32 bp long, encompassing the substitution sites ("mutagenic" primers), and terminal primers. In a first step, overlapping mutagenized fragments were amplified in separate PCR reactions using pairs of mutagenic primers, or a mutagenic primer and a terminal primer for terminal fragments. In a second step, purified overlapping products from the previous steps were assembled and amplified using terminal primers only. Modified LFAH12 genes containing one or seven substitutions were constructed using native-wildtype (WT) coding sequences as templates in the first PCR step.

Modified LFAH12 genes containing only six mutations were constructed using a gene substituted at all seven codons (mLFAH12) as a template. The 5'-end of terminal primers was modified to allow the introduction of convenient restriction sites for the cloning of PCR products. Two sets of PCR "mutagenic" primers were constructed to modify the LFAH12 gene. In the first

set (mH1-5,mH67), the oligonucleotides contained one or two mismatches to modify a target codon(s) in the WT sequence. In the second set (H1-7), the primers contained no mismatch with the WT sequence, and were designed for the substitution of a WT codon for a mutant codon in mLFAH12. In the case of FAD2, only one set of oligonucleotides was synthesized (mD1-5,mD67) which was designed for the modification of the WT gene (Table 1). By genetic engineering, modified desaturase or hydroxylase genes containing each of the seven mutations may be recombined to produce any combination of two, three, four, five or six mutations. As shown below, such modified genes will exhibit varying degrees of metabolic activities.

#### 10 PCR Conditions:

First step: 10 ng of plasmid DNA was added to a PCR reaction containing 200  $\mu$ M dNTPs, 100 mM KCl, 100 mM  $(\text{NH}_4)_2\text{SO}_4$ , 200 mM Tris-HCl (pH 8.8), 20 mM  $\text{MgSO}_4$ , 1% (v/v) Triton X-100, 1000  $\mu$ g/ml BSA, 3 mM  $\text{MgCl}_2$ , 5% (v/v) DMSO, 125 pmol of each primer, 1.25 units of cloned *Pfu* polymerase (Stratagene), to a final volume of 50  $\mu$ l. Amplifications conditions were: 4 min denaturation step at 94°C, followed by 30 cycles of 92°C for 1 min, 50°C for 1 min, 72°C for 2 min, concluded with a final extension step at 72°C for 5 min. PCR products were run on and purified from agarose or polyacrylamide gels.

Second step: 10 ng of purified overlapping fragments were used as templates in PCR reactions similar to the above. Amplification conditions were identical except that products were amplified for only 15 cycles.

#### Cloning Strategy:

PCR fragments encoding modified LFAH12 enzymes were cloned into pBluescriptKS-derived plasmids using one of two general strategies, depending on the location in the molecule of the nucleotides to be substituted. In these approaches, advantage was taken of a unique *Pst*I site near the middle of the coding sequence and that *Pfu* polymerase generates blunt-ended fragments.

If the nucleotide substitutions to be introduced were 5' of the *Pst*I site, overlapping fragments were assembled using terminal primers H5' and mH4r. The resulting products were purified then cut with *Pst*I. In a second step, the pBluescript-derived pLFAH12-1 plasmid (ref) was cut with *Eco*RV and *Pst*I, and the vector fragment was purified and ligated to the cut PCR fragment. If the nucleotide substitutions to be introduced were located 3' of the *Pst*I site, overlapping fragments were assembled using mH3f and H3', cut with *Pst*I, then ligated to the vector fragment from a digest of pLFAH12-1 with *Pst*I and *Sma*I. Alternatively, the assembled

PCR products were cut with *Pst*I and *Sac*I, then ligated to the vector fragment from a restriction digest of pLFAH12-1 with the same enzymes.

Similar strategies were followed to obtain clones containing LFAH12 sequences modified at six out of seven residues, except that mLFAH12 (which encodes a LFAH12 enzyme modified at seven residues) was first substituted for LFAH12 in the vector pLFAH12-1, using the strategies  
5 described above, resulting in the vector pmLFAH12. If the nucleotides to be substituted in pmLFAH12 were 5' of the central *Pst*I site, the vector was cut with *Stu*I and *Pst*I and the insert fragment was substituted for appropriate PCR-assembled fragments cut with *Pst*I. If the nucleotide substitutions to be introduced were 3' of the *Pst*I site, pmLFAH12 was cut with *Pst*I  
10 and *Sac*I, the vector fragment was purified, then ligated to appropriate PCR fragments cut with the same enzymes. All inserts were sequenced to confirm the presence of the expected nucleotide substitutions and the absence of secondary mutations which can arise from PCR amplification.

Yeast expression vectors containing WT or modified LFAH12 genes were constructed by excising inserts from the above constructs using the enzymes *Hind*III and *Sac*I, and cloning them  
15 into the bacterial-yeast shuttle vector pYESII (Invitrogen), cut with the same enzymes. For the construction of binary vectors for plant transformation, pBI121 was cut with *Sma*I and *Sac*I, and the resulting vector fragment was purified. In a second step, inserts were excised from the pBuescriptKS-derived plasmids described above using the enzymes *Stu*I and *Sac*I, and substituted for the GUS gene in the pBI121 vector.

20 *A. thaliana* cDNA 146 M12T7 encoding FAD2 was obtained from the Arabidopsis Stock Center at the Ohio State University. This cDNA sequence was amplified using the *Pfu* DNA polymerase in conjunction with primers D5' and D3' to introduce the flanking restriction sites, *Kpn*I and *Sma*I immediately preceding the initiation codon ATG, and *Sac*I and *Eco*RI restriction sites following the terminator codon TGA. This amplified wild type FAD2 fragment was cloned  
25 into the *Eco*RV site in the vector pZerO (Invitrogen). For expression of FAD2 in yeast, the insert was then excised by restriction with *Kpn*I and *Eco*RI and cloned into the corresponding sites in the bacterial-yeast shuttle vector pYESII (Invitrogen), resulting in the plasmid pYESII-F2. The binary vector pDN was constructed for seed-specific expression of the WT and modified FAD2 genes in plants. In a first step, the napin promoter was amplified from rapeseed DNA using the  
30 oligonucleotide primers nap1 (GGCGTCGACAAGCTTCTGCGGATCAAGCAGCTTTCA) and nap2 (GGTTTTGAGTAGTGATGTCTTGTATGTTCTAGATGGTACCGTAC). In a second step, a *Hind*III-*Bgl*III fragment carrying the napin promoter was substituted for the 35S promoter by cutting the pBI121 plasmid (Clontech) with *Hind*III and *Bam*HI. A separate excision of the

FAD2 insert was made using the restriction enzymes *Sma*I and *Sac*I. This fragment was cloned into pDN using corresponding restriction sites.

The construction of the mFAD2 cDNA encoding a modified FAD2 enzyme containing seven amino acid substitutions was achieved using overlap extension PCR. Following the second round of assembly-amplification using the primers D5' and D3', the PCR products were treated exactly as the amplified wild type FAD2 sequence described above with respect to the construction of vectors for expression in yeast and in plants. Once again, all inserts were sequenced to confirm the presence of the expected nucleotide substitutions and the absence of secondary mutations which can arise from PCR amplification.

10

#### Enzyme Assays:

Root microsomes were prepared as in Miquel and Browse (1992), with some modifications: the extraction buffer contained 2.5 mM NADH and catalase was 10,000 U/ml instead of 2,000 U/ml. After centrifugation at 100,000 g, microsomal membranes were rinsed in desaturase reaction buffer (also containing 10,000 U/ml catalase) before being dispersed in the same buffer to a final concentration of ~0.5 mg/ml microsomal protein. The membranes were then incubated in the presence of 85,000 dpm <sup>14</sup>C-oleoyl CoA (52 Ci/mol), and the labeled lipids were extracted after addition to the reaction of an equal volume of 2 M NaCl, 0.2 N HCl and 2 ml of chloroform/methanol (1:1). The chloroform phase was recovered, dried under nitrogen, and the fatty acids were transmethylated in 1 N methanolic HCl for 1 h at 80°C. After addition of an equal volume of 0.9% NaCl, the fatty acid methyl esters (FAME) were extracted into hexane. The hexane was subsequently evaporated under nitrogen, and the FAME were redissolved in 50 ml chloroform. The FAME were then separated along side standards by argentation TLC as in Miquel and Browse (1992), using hexane/ethyl ether (80:20) as the mobile phase. After drying, the plates were exposed to PhosphorImager cassettes, and the radioactivity of target fame's was measured by comparison to known quantities of labeled fatty acids spotted on the plate.

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#### Protein Quantitation:

Proteins were quantitated using Bradford assay reagents (Biorad) or a TCA kit (Pierce) with known amounts of BSA as a standard.

30

#### Gene Expression in Yeast:

Yeast strain INVCS2 (InVitrogen) was electroporated with expression constructs and

control vector. Transformed cells were selected on SC-ura plates (obtained from Bio 101) containing 2% glucose. Resulting colonies were used to inoculate SC-ura liquid medium containing 2% galactose. Stationary phase cells were diluted to an OD<sub>600</sub> of 0.5 in fresh medium, and grown for 5 days at 16°C. The cultures were then centrifuged and pellets were assayed for fatty acid content.

#### Plant Transformation:

Transgenic plants were generated using a modified *in planta* transformation procedure (Bectold et al., 1993). Batches of 12 to 15 plants were grown on soil covered with nylon screens for 3 to 4 weeks under continuous light (100 mmol m<sup>-2</sup>s<sup>-1</sup> irradiation in the 400 to 700 nm range). Primary bolts were removed four days before use to promote growth of multiple secondary bolts. *Agrobacterium tumefaciens* strain GV3101 carrying binary Ti plasmid derivatives was grown in liquid cultures to stationary phase in LB medium with 15 mg/l gentamycin and 50 mg/l kanamycin. Cells were harvested and resuspended in infiltration medium (Murashige and Skoog macro and micronutrient medium containing 10 mg/l 6-benzylaminopurine and 5% glucose). Plants were immersed in the bacterial suspension, then placed under vacuum (600 mm Hg) until tissues appeared uniformly soaked. Infiltrated plants were grown at 25°C under continuous light for four weeks. Seeds, bulk harvested from each pot, were sterilized in a mixture of bleach, water and Triton X-100 (30%, 70%, 0.1%), then germinated on selective medium (1 X Murashige and Skoog salts medium enriched with B5 vitamins, with 50 mg/l kanamycin). Kanamycin resistant seedlings (the T1 generation) were transferred to soil to produce T2 seed.

#### Measurements of Fatty Acid Composition:

For analysis of seed fatty acid composition, seeds were harvested from dry siliques and the fatty acid composition was determined from lipids extracted from pools of 50 seeds. For analyses of yeast fatty acid composition, cell pellets from 15 ml cultures were extracted in the same way as seed samples.

Fatty acids from samples were transmethylated in 1 ml of 1N methanolic HCl (80°C, 1 hour) and extracted twice into hexane after addition of an equal volume of aqueous 0.9% NaCl. Fatty acid methyl esters were derivatized with BSTFA/TMCS (99:1) at 70°C for 30 min in order to obtain trimethylsilyl fatty acid methyl esters (TMS-FAME) of hydroxylated fatty acids. Fatty acids were resolved on an SP2340 fused silica capillary column (0.25 mm ID, 60 m, Supelco) in splitless mode using 1 ml/min of helium. The injector and detector temperatures were 300°C; the

temperature program was 100 to 160°C at 25°C min, 160 to 240°C at 7°C min, hold at 240°C for 5 min then decrease to 100°C at 25 min. The identity of fatty acids in the samples was determined by comparing retention times and mass spectra to that of standards. A Hewlett-Packard HP5971 MS was used to confirm the identity of eluting compounds.

- 5           For the analysis of the composition of individual lipid classes, lipids were extracted as in Miquel and Browse (1992).

Example 1: Modification of a desaturase to a hydroxylase.

- 10           Evidence that a desaturase can be converted into a synthetic hydroxylase was obtained by modifying the FAD2 delta-12 oleate desaturase from *A. thaliana* so that it exhibited hydroxylase activity. The nucleotide sequence and corresponding amino acid sequence of the *A. thaliana* FAD2 gene is shown in Figure 3.

- 15           A modified version of the FAD2 cDNA encoding seven mutations of the coding sequence and introduction of flanking mutations was achieved using a method based on overlap-extension PCR described by Ho et al. (1989). Briefly, two rounds of PCR are employed (Figure 4). In the first round, in a series of separate PCR reactions, individual fragments designated "A" to "G" are amplified that are tailed by the desired mutated DNA sequence using the wild type *A. thaliana* FAD2 DNA as template and various pairs of oligonucleotide primers encoding the desired DNA  
20           mutations. For instance, primers mD1f and mD1r (Table 1) were used in one reaction to amplify a fragment. Similarly, primers mD2f and mD2r (Table 1) are used in a second reaction, mD3f and mD3r are used in a third reaction, mD4f and mD4r are used in a fourth reaction, mD5f and mD5r are used in a fifth reaction and mD67f and mD67r are used in a sixth reaction. The primer pair mD67f and mD67r introduced two amino acid substitutions.

- 25           The amplified fragments are then separated from the DNA template by excision and elution from a 5% acrylamide gel. A portion of the purified fragments A-G are pooled into a single PCR reaction and are used as the DNA template in an amplification employing only flanking oligonucleotides D5' and D3' (Table 1). In the first few cycles of amplification, various pairs of DNA fragments overlap and become extended until a continuous template is assembled  
30           and subsequently the flanking primers allow for amplification of the entire gene containing all the mutations encoded in the original oligonucleotide primers. It should be emphasized that the fragments are used as a template in the second round of PCR and that full length DNA template is only included in the first round PCR reactions. Following this second round of assembly-

amplification, the fragment is treated exactly as the amplified wild type FAD2 sequence described above with respect to its analysis and introduction into yeast and plants for analysis.

The nucleotide sequence of the mFAD2 gene is presented as SEQ ID NO:1. The amino acid sequence of the polypeptide product of the mFAD2 gene is presented as SEQ ID NO:2. A comparison of the nucleotide sequences of the FAD2 and mFAD2 genes is presented in Figure 5. A comparison of the deduced amino acid sequences of the polypeptide products of the FAD2 gene and the mFAD2 gene is presented in Figure 6.

In order to evaluate the effect of the introduced mutations on the activity of FAD2, the modified gene was expressed in yeast. In yeast, FAD2 is active and causes the accumulation of linoleate. Wild-type cells, which do not have this enzymatic activity, do not accumulate this fatty acid. In the present experiment, the mutant desaturase gene (mFAD2) was cloned into the pYESII vector downstream of the GAL1 promoter and electroporated into yeast cells. Transgenic cells were grown under conditions that led to expression of the gene, were harvested and their fatty acid composition determined by gas chromatography. As shown in Table 2, there were dramatic differences between the fatty acid phenotypes of cells expressing the mutant and wild-type genes.

Table 2. Fatty acid composition of wild-type yeast, yeast containing the FAD2 gene and yeast containing the mFAD2 gene. The values are average values for five independent transformants. Standard errors are shown in parentheses.

Fatty acid (mol % of total fatty acids)			
Line	16:2	18:2	18:1-OH
WT	0.00	0.00	0.00
FAD2	0.58 (0.23)	3.52 (0.57)	0
mFAD2	0.4 (0.17)	1.37 (0.23)	0.51 (0.11)

In cells expressing FAD2, hydroxylated fatty acids were not detectable. However, cells expressing mFAD2 accumulated ricinoleic acid, which constituted on average 0.5% of total fatty acids. Concurrently, their average linoleate content was 1.4% of total fatty acids as compared to 3.5% in cells expressing the unmodified FAD2 gene. Based on the sensitivity of the assay, we  
5 estimate that the effect of the mutations was to increase the ratio of ricinoleate to linoleate content at least 13-fold in transgenic cells. Thus, the seven amino acid differences between FAD2 and mFAD2 convert the enzyme from a desaturase to a synthetic hydroxylase that has both desaturase and hydroxylase activity.

In order to verify that the synthetic hydroxylase was also useful for production of  
10 hydroxylated fatty acids in plants, the mutant gene was expressed in transgenic *A. thaliana* plants. In order to detect the lowest possible levels of hydroxylase activity while still measuring oleate desaturation, mFAD2 was expressed in the FAD2 mutant of *A. thaliana* under the control of the strong seed-specific promoter from the *B. rapa* napin gene. We also obtained 15 transgenic lines expressing the wild-type FAD2 desaturase gene. Accumulation of hydroxylated fatty acids was  
15 never detectable in the seeds of these plants. Eight transgenic lines expressing mFAD2 were examined (Table 3).

Table 3. Seed fatty acid composition of transgenic *A. thaliana* FAD2 mutant plants expressing the mFAD2 gene. The transgenic plants containing the mFAD2 gene were designated MF2-1 to MF2-8, respectively (average of two measurements on 25 T2 seeds).

5

Fatty Acid (mol % of total fatty acids)										
Line	16:0	18:0	18:1	18:2	18:3	20:0	20:1	18:1-OH	18:2-OH	20:1-OH
FAD2*	6	3	40	5	7	1.5	15.2	0	0	0
MF2-1	5.65 (0.07)	3.3 (0.14)	42.1 (2.19)	10.8 (1.83)	12.5 (0.14)	1.4 (0)	20.25 (0.49)	1.35 (0.35)	1.65 (0.35)	0.25 (0.07)
MF2-2	7.25 (0.21)	4.05 (0.21)	28.85 (2.19)	19.8 (1.97)	15.4 (0.84)	1.4 (0)	15.95 (1.62)	2.75 (0.49)	2.4 (0.28)	0.7 (0.14)
MF2-3	5.85 (0.21)	3.2 (0)	34.15 (2.33)	18.3 (1.13)	15.9 (0.28)	1.0 (0)	15.85 (0.49)	2.5 (0.42)	2.85 (0.49)	0.6 (0.14)
MF2-4	6.75 (0.35)	4.7 (0.28)	29.55 (0.49)	23.3 (1.13)	10.55 (0.49)	1.3 (0.14)	13.3 (0.14)	3.45 (0.35)	2.1 (0.42)	0.9 (0.14)
MF2-5	7.65 (0.21)	4.05 (0.21)	27.35 (3.46)	17.95 (1.76)	15.05 (0.49)	1.65 (0.21)	18.25 (1.06)	2.7 (0.56)	3.4 (0.28)	0.7 (0.14)
MF2-6	7.9 (0.42)	4.15 (0.21)	29.3 (2.19)	23.1 (3.53)	13.45 (1.34)	8.8 (0.14)	6.95 (2.75)	3.5 (0.7)	2.4 (0.14)	0.95 (0.07)
MF2-7*	8.3	5	21.7	25	14.1	1.7	13.5	4.9	3	1.3
MF2-8	8.55 (0.35)	4.8 (0.14)	19.45 (2.33)	29.4 (0)	11.9 (0.14)	1.45 (0.07)	12.1 (0.28)	4.75 (0.21)	3.2 (0.28)	1.45 (0.07)

\* Replicates were not done for these samples

10 In contrast with transgenic plants expressing the WT gene, the proportion of hydroxylated fatty acids, which included ricinoleic and derivatives densipolic and lesquerolic acids, ranged from 3.2% to 9.4% ( $6.7\% \pm 1.9\%$ ) of total seed fatty acids. The ratio of seed linoleate to oleate contents were 2 to 12 times higher ( $6.4 \pm 3.1$ ), which indicated significant desaturase activity, albeit lower than in the seeds of plants transformed with the WT gene. The levels of hydroxylated fatty acid accumulation observed in transgenic plants expressing mFAD2 indicate that all or part  
15 of the amino acid substitutions were sufficient to promote significant levels of hydroxylase activity *in planta*. However, these changes did not have the effect of eliminating desaturase

activity of the enzyme.

We envision that one skilled in the art may obtain similar or identical results by practicing minor variations of the invention disclosed herein. One class of modifications is to simply make the corresponding changes in a plant oleate desaturase other than the FAD2 gene from *A.*

5 *thaliana*. Because of the high degree of sequence conservation among plant microsomal oleate desaturases, identification of other desaturases and their modification by mutagenesis could be performed by the skilled artisan. Another minor variation of this invention would be to omit one or more of the seven amino acid substitutions we have used.

Because of the results disclosed in Example 2, we envision that enzymes with similar or  
10 identical properties could be obtained by making only two, three, four, five, or six mutations at the amino acid positions disclosed herein. The minimal set could be identified by systematically making all seven combinations of synthetic hydroxylase enzymes with six out of seven substitutions. In the next step, all of the synthetic hydroxylases with six substitutions that had acceptable levels of hydroxylase activity would be used to design a series of synthetic hydroxylase  
15 enzymes with all six combinations of five substitutions and so on until the minimal set of substitutions that gave acceptable activity were identified. We also envision that it may be possible to make synthetic hydroxylase enzymes with similar or identical properties by making more than seven substitutions that included neutral substitutions chosen at random or by comparison of the range of natural variation in desaturases and hydroxylases. We also envision  
20 that it may be possible to produce synthetic hydroxylases with similar or identical properties to the enzyme disclosed herein by making different amino acid substitutions at some or all of the seven sites used herein. For example, instead of converting the alanine at position 63 to Valine (mutation A63V), it might be equally effective to convert alanine-63 to isoleucine or leucine. These and other variations on the present invention may be performed by the one of skill in the  
25 art.

#### Example 2: Conversion of a hydroxylase to a desaturase.

30 In order to increase the ratio of oleate desaturation to oleate hydroxylation catalyzed by the oleate hydroxylase gene from *L. fendleri* (LFAH12), overlap extension PCR with high-fidelity *Pfu* polymerase was used to introduce nucleotide substitutions in the coding region of the LFAH12 gene. As in Example 1, six pairs of mutagenesis primers (designated mH1f to mH67r in

Table 1) were used in combination with terminal primers to amplify fragments which were then assembled in a second PCR amplification step to produce modified full-length coding sequences. The modified gene was designated mFAH12.

5 The nucleotide sequence of the mFAH12 gene is listed as SEQ ID NO:3. The deduced amino acid sequence of the polypeptide product of the mFAH12 gene is listed as SEQ ID NO:4. A comparison of the nucleotide sequence of the FAH12 and mFAH12 genes is presented as Figure 7. A comparison of the deduced amino acid sequences of the FAH12 and mFAH12 genes is presented as Figure 8.

10 In order to evaluate the effect of the introduced mutations on the activity of LFAH12, we expressed the modified genes in yeast. In yeast, LFAH12 is active and causes the accumulation of ricinoleate. Wild-type cells do not accumulate ricinoleate. In the present experiment, the mutant hydroxylase gene (mLFAH12) was cloned into the pYESII vector downstream of the GAL1 promoter and electroporated into yeast cells. Induced transgenic cells were harvested and their fatty acid composition determined by gas chromatography. As shown in Table 4, there were  
15 dramatic differences between the fatty acid phenotypes of cells expressing the mutant and wild-type genes.

Table 4. Fatty acid composition of wild-type yeast, yeast containing the LFAH12 gene and yeast containing the mLFAH12 gene (average values for five independent transformants).

Fatty Acid (mol% of total fatty acids)			
Line	16:2	18:2	18:1-OH
WT	0.00	0.00	0.00
LFAH12	0.74 (0.16)	0.65 (0.03)	1.52 (0.18)
mLFAH12	2.69 (0.27)	6.17 (0.99)	0.33 (0.04)

5

Although desaturase activity of the LFAH12 enzyme is minor compared to its hydroxylase activity, yeast cells expressing LFAH12 accumulate linoleic and ricinoleic acids to similar levels, possibly because linoleic acid is tolerated better than ricinoleic acid, a phenomenon also observed in plant cells. In cells expressing mLFAH12, the ratio of linoleic to ricinoleic acid was on average 43-fold higher than in cells expressing the wild-type gene. There was also a 4-fold increase in the levels of 16:2, which is the product of palmitoleic acid desaturation. These observations suggest a significant increase in desaturase activity associated with a decrease in hydroxylase activity upon introduction of the seven modified amino acid residues in mLFAH12.

To measure the effect of the amino acid substitutions on desaturase activity of the LFAH12 enzyme in plants, mLFAH12 was introduced into the *A. thaliana* FAD2 mutant, which is deficient in oleate desaturation. In transgenic FAD2 plants where LFAH12 is driven by the strong CaMV35S promoter, hydroxylated fatty acids accumulate to high levels, while the mutant phenotype is partially suppressed in roots, due to low levels of desaturase activity of the enzyme. mLFAH12 was expressed under the control of the same promoter and the fatty acid composition of leaves and seeds of transgenic plants was measured.

Table 5. Seed fatty acid composition of transgenic *A. thaliana* FAD2 mutant plants expressing the mFAH12 gene. The transgenic plants containing the mFAH12 gene were designated MH2-1 to MH2-8, respectively (Average of two measurements on 25 T2 seeds)

5

## Fatty Acid (mol% of total fatty acids)

Line	16:0	16:3	18:0	18:1	18:2	18:3
FAD2	13.75 (0.68)	19.75 (2.12)	0.51 (0.05)	7.78 (1.14)	2.08 (0.33)	44.68 (0.74)
MH2-1*	14.2	13.2	1	9.1	5	49.4
MH2-2*	12.5	15.7	1.8	5.3	10.8	41.4
MH2-3*	13.3	10.8	0.5	3	10.4	58.7
MH2-4	14.2 (0.7)	15.35 (1.06)	0.75 (0.35)	2.85 (0.77)	4.65 (0.49)	55.5 (0.56)
MH2-5	14.35 (0.35)	12.65 (1.76)	0.85 (0.21)	2.15 (1.62)	10.7 (1.69)	58.1 (5.65)
MH2-6	14.05 (0.21)	17.9 (0.84)	1.05 (0.07)	1.0 (0.28)	7.2 (0.42)	51.65 (2.05)
MH2-7	13.35 (0.77)	19.45 (1.2)	0.65 (0.21)	0.9 (0.14)	6.55 (0.21)	58.75 (0.91)
MH2-8	15.85 (0.35)	15.3 (2.54)	1.0 (0)	0.75 (0.35)	8.0 (0.98)	53.6 (0)
MH2-9	18.65 (0.91)	16.8 (1.27)	1.0 (0)	0.5 (0)	5.85 (0.49)	55.65 (0.91)
MH2-10	12.05 (0.77)	19.3 (0.56)	0.5 (0)	0.4 (0.14)	5.35 (0.21)	54.15 (5.72)

In contrast with plants expressing the WT gene which always show a characteristic mutant leaf fatty acid phenotype, expression of mFAH12 in the FAD2 mutant resulted in suppression of the leaf phenotype in eight out of the 10 transgenic plants which were analyzed in Table 5.

10 Furthermore, analysis of the root fatty acid composition of one of these transgenic lines revealed

that the mutant phenotype was also completely suppressed in this tissue. In addition, hydroxylated fatty acids were not detected in the seeds of any of the transgenic plants. However, expression of mLFH12 resulted in an increase of the ratio of linoleate to oleate content 5 to 10 times ( $7.6 \pm 2.7$ ) over untransformed plants. From this data, which is consistent with the yeast results, we can conclude that expressing mLFAH12 in plants deficient in oleate desaturation has similar phenotypic consequences as expressing a desaturase encoding gene such as FAD2.

We also evaluated the contribution of each of the seven amino acid substitutions to the overall effect of the mutations on the activity of the hydroxylase. We constructed seven modified LFAH12 genes substituted at only six of seven residues, expecting that if the change in enzymatic activity was due for a major part to a single residue, an enzyme with no substitution at this residue would have close to WT activity. Vectors containing each of the seven constructs were introduced into yeast cells, and the accumulation in these cells of ricinoleic and polyunsaturated fatty acids was measured. As shown in Table 6, the fatty acid profiles of cells expressing the different mutant genes was very similar to cells expressing LFAH12.

Table 6. Fatty acid composition of wild-type yeast, yeast containing the LFAH12 gene, yeast containing the mLFAH12 gene and yeast containing mLFAH12 genes substituted at six out of the seven residues. Values given are average values for five independent transformants. Standard errors are given in parentheses.

Line	Fatty acid		
	16:2	18:2	18:1-OH
mol% of total fatty acids			
WT	0.00	0.00	0.00
LFAH12	0.74 (0.16)	0.65 (0.03)	1.52 (0.18)
mLFAH12	2.69 (0.27)	6.17 (0.99)	0.33 (0.04)
mLF-V63A	3.08 (0.45)	6.98 (0.84)	0.39 (0.04)
mLF-G105A	2.31 (0.17)	5.73 (0.85)	0.47 (0.06)
mLF-N149T	1.65 (0.09)	3.89 (0.48)	0.63 (0.06)
mLF-F218Y	1.85 (0.19)	4.87 (0.48)	0.42 (0.15)
mLF-V296A	1.84 (0.03)	4.22 (0.2)	0.94 (0.03)
mLF-A323S	2.12 (0.16)	4.75 (0.83)	0.39 (0.04)
mLF-I325M	2.76 (0.11)	5.28 (0.36)	0.43 (0.03)

This result indicates that introducing a single WT residue in mLFAH12 is not sufficient to restore the WT activity of the enzyme. In order to eliminate the possibility that more than one residue substitution could alone account for the full effect, we tested the effect of introducing single FAD2 residues in the WT enzyme. From the fatty acid phenotype of transgenic yeast cells  
5 expressing the seven mutant genes obtained, none of the mutant enzymes had activities which differed significantly from the WT enzyme.

The above experiment indicates that changing the activity of the *L. fendleri* hydroxylase requires introducing multiple amino acid substitutions in the enzyme. We propose that in the *L. fendleri* hydroxylase, and also in the *A. thaliana* desaturase, a subset of seven residues act  
10 together to determine the ratio of desaturase to hydroxylase activities of the enzyme. Because of their proximity to putative iron binding sites, we envision that these residue influence the conformation of the active site. Altering this conformation by introducing key amino acid substitutions would result in affecting the outcome of the overall reaction.

Subsequent experiments to identify amino acid residues that may be responsible for the  
15 conversion of the ubiquitous oleate desaturase into an oleate hydroxylase were conducted by again comparing the deduced amino acid sequences of the hydroxylases from *L. fendleri* and *R. communis* with the sequences for oleate desaturases from *Arabidopsis*, *Zea mays*, *Glycine max* (two sequences) and *R. communis*. Additionally, comparison was also made with the sequence for oleate desaturase from *Brassica napus*. This series of comparisons also revealed that there  
20 were only seven residues that were strictly conserved in all of the six desaturases but divergent in both of the available hydroxylases. Four of the residues were adjacent to the conserved histidine clusters. Similar to the initial experiments, the role of these seven residues was assessed by using site-directed mutagenesis to replace the residues found in the *Lesquerella* hydroxylase, LFAH12, with those from the equivalent positions in the desaturases. The seven mutations were V63A,  
25 G105A, N149T, F218Y, V296A, A323S, I325M numbered relative to the LFAH12 sequence.

Mutagenic oligonucleotides were used to introduce nucleotide substitutions into cloned genes by overlap-extension PCR (W. Ito, H. Ishiguro, Y. Kurosawa, *Gene* 102, 67 (1991)). In a first step, overlapping fragments were amplified in separate PCR reactions using primer pairs designed to introduce mutations. The products were gel-purified, then assembled in a PCR  
30 reaction primed with terminal primers only. Modified LFAH12 genes containing one or seven substitutions were constructed using pLFAH12-1 as template and primers mH1-5 or mH67. Modified LFAH12 genes containing only six mutations were constructed using m<sub>7</sub>LFAH12 as a template and one of primers H1-H7 to revert one of the mutations. The 5'-end of terminal primers

was modified to allow the introduction of convenient restriction sites for the cloning of PCR products. The m<sub>7</sub>FAD2 was constructed using oligonucleotides D1-5, D67.

The PCR conditions were: 10 ng of plasmid DNA, 200 μM dNTPs, 100 mM KCl, 100 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 200 mM Tris-HCl (pH 8.8), 20 mM MgSO<sub>4</sub>, 1% (v/v) Triton X-100, 1000 μg/ml  
 5 BSA, 3 mM MgCl<sub>2</sub>, 5% (v/v) DMSO, 125 pmol of each primer, 1.25 U of Pfu polymerase (Stratagene), to a final volume of 50 μl. Amplification conditions were: 4 min denaturation step at 94° C, followed by 30 cycles of 92° C for 1 min, 50° C for 1 min, 72° C for 2 min, concluded with a final extension step at 72° C for 5 min. PCR products were purified from agarose or polyacrylamide gels. For the second PCR step 10 ng of purified overlapping fragments were used  
 10 as templates in PCR reactions as above except that only 15 cycles were used.

PCR fragments encoding modified LFAH12 enzymes were cloned into pLFAH12-1 cut with *PstI* and one of *SmaI* or *EcoRV* or *SacI*. All inserts were sequenced. Yeast expression vectors containing WT or modified LFAH12 genes were constructed by excising inserts from the above constructs using the enzymes *HindIII* and *SacI*, and cloning them into the *HindIII-SacI* sites  
 15 of pYESII (Invitrogen). Constructs for plant transformation were made by cloning the *StuI-SacI* fragment from modified LFAH12 genes into the *SmaI-SacI* sites of pBI121.

The FAD2 cDNA clone 146M12T7 was amplified with Pfu DNA polymerase using primers D5' and D3' to introduce restriction sites for *KpnI* and *SmaI* immediately upstream of the initiation codon, and *SacI* and *EcoRI* restriction sites following the terminator codon. The  
 20 fragment was cloned into the *EcoRV* site in the vector pZER0 (Invitrogen). For expression of FAD2 in yeast, the insert was excised by restriction with *KpnI* and *EcoRI* and cloned into the corresponding sites in the pYESII, resulting in plasmid pYESII-F2. Binary Ti-vector pDN was constructed for seed-specific expression of FAD2 genes. In a first step, the napin promoter was amplified from rapeseed DNA using primers ggcgtcgacaagcttctgcggatcaagcagcttca and  
 25 gggtttgagtagtgatgtctgtatgttctagatggtaccgtac. A *HindIII-BglII* fragment was cloned into the *HindIII-BglII* sites of pBI121 (Clontech), replacing the 35S promoter. FAD2 coding sequences were excised from pYESII-F2 with *SmaI* and *SacI* and cloned into pDN using corresponding restriction sites.

The construction of the m<sub>7</sub>FAD2 cDNA encoding a modified FAD2 enzyme containing  
 30 seven amino acid substitutions was achieved using overlap extension PCR. Following the second round of assembly-amplification using the primers D5' and D3', the PCR products were treated exactly as the amplified wild type FAD2 sequence described above.

Plant expression constructs were introduced into *Agrobacterium tumefaciens* strain

GV3101 pMP90 using electroporation and used to transform Arabidopsis *fad2* mutant plants by vacuum infiltration (D. Bouchez, C. Camilleri, M. Caboche, *Comptes Rendus De L'Academie Des Sciences Serie Iii* 316, 1188 (1993) ). The oligonucleotides used were the same as those earlier described Table 1.

5 In a reciprocal experiment, the seven residues in the Arabidopsis FAD2 oleate desaturase were replaced with the corresponding *Lesquerella* hydroxylase residues. The seven mutations were A63V, A105G, T148N, Y217F, A296V, S322A, M324I based on the numbering of the Arabidopsis FAD2 sequence. The activity of the modified and unmodified genes was then determined by expressing them in yeast and transgenic plants, before analyzing the composition of  
10 the total fatty acids. Technical difficulties limited the utility of direct measurements of enzyme activity in cell extracts. The enzymes are integral membrane proteins that act on fatty acids esterified to lipids and require cytochrome  $b_5$  reductase and cytochrome  $b_5$  for activity. The difficulty of quantitatively incorporating labeled lipids into isolated membranes, and ensuring that cytochrome  $b_5$  and  $b_5$  reductase are not limiting, restricts the utility of direct measurements of  
15 enzyme activity. Our best estimates of oleate desaturase or oleate hydroxylase activities in crude microsomal preparations from Arabidopsis roots indicated specific activities of 1.2 and 0.3 pmol/mg protein/min, respectively.

The mutant hydroxylase and desaturase genes containing all seven substitutions (designated  $m_7$ LFAH12 and  $m_7$ FAD2, respectively) were expressed in yeast cells under  
20 transcriptional control of the GAL1 promoter. Transgenic cells were harvested after induction and their total fatty acid composition determined by gas chromatography. Wild-type yeast cells do not accumulate detectable levels of diunsaturated or hydroxylated fatty acids (Covello et al. and Kajiwarra et al.). The results are shown in Table 7 and presented graphically in Figure 9. Cultures were induced in growth medium containing galactose,  $\sim 2 \times 10^8$  cells were harvested, and fatty  
25 acids were extracted and modified for analysis by gas chromatography, as described by Broun et al., 1998. Values are the averages ( $\pm$  SE) obtained from five cultures of independent transformants. Expression of FAD2 caused the accumulation of about 4% of diunsaturated fatty acids (16:2 and 18:2) but no detectable hydroxy fatty acids. Expression of LFAH12 caused the accumulation of about 1.4% diunsaturated fatty acids and 1.5% ricinoleic, confirming the mixed  
30 function of this enzyme (Broun et al., 1998). Cells expressing  $m_7$ FAD2 accumulated ricinoleic acid to  $\sim 0.5\%$  of total fatty acids and had  $\sim 50\%$  reduction in the accumulation of diunsaturated fatty acids. Thus, replacement of the seven residues converted a strict desaturase to a bifunctional desaturase/hydroxylase comparable in activity to the unmodified *Lesquerella* hydroxylase.

The amount of desaturase activity of the LFAH12 enzyme is relatively low compared to its hydroxylase activity (Broun et al., 1998). However, yeast cells expressing LFAH12 accumulated linoleic and ricinoleic acids to similar levels, possibly because linoleic acid is more stable than ricinoleic acid in yeast cells. In cells expressing m<sub>7</sub>LFAH12, the ratio of 18:2 to ricinoleic acid was on average 43-fold higher than in cells expressing LFAH12. There was also a 16-fold increase in the ratio of 16:2 to ricinoleic acid. Thus, there was both a major increase in desaturase activity and a decrease in hydroxylase activity upon introduction of the seven desaturase-equivalent residues into LFAH12.

Table 7

% Total Fatty Acids/Fatty Acid

gene	Line	16:2	18:2	R*
	FAD2	0.58	3.52	0.00
	M7FA22	0.40	1.37	0.51
	LFAH12	0.74	0.65	1.52
	m7LFAH12	2.69	6.17	0.33

\*Ricinoleate

The activity of the mutant enzymes *in planta* was examined by using the corresponding genes to produce stable transgenic plants in an Arabidopsis *fad2* mutant which is deficient in oleate desaturase activity (Miguel et al., 1992). The results are shown in Table 8 and presented graphically in Figure 10. Measurements were made of the fatty acid composition of leaf lipids from wild type, the *fad2* mutant, and transgenic *fad2* plants expressing LFAH12 or m<sub>7</sub>LFAH12, under the control of the CAMV 35S promoter. Values at means  $\pm$  SE (n=3). Expression of LFAH12 under transcriptional control of the constitutive CAMV 35S promoter resulted in accumulation of high levels of hydroxy fatty acids in seeds, but no detectable suppression of the *fad2* mutant phenotype in leaves. By contrast, expression of m<sub>7</sub>LFAH12 under the same circumstances resulted in complete suppression of the *fad2* phenotype in 8 out of 10 transgenic plants analyzed. There was an average 21-fold increase in the ratio of linoleate to oleate in leaf fatty acids and a small increase in the amount of linolenic acid. These results, which are consistent with the results of the yeast assays, confirm that expression of m<sub>7</sub>LFAH12 in plants deficient in oleate desaturation has identical phenotypic consequences to expressing a wild type desaturase such as FAD2 (Miguel et al., 1992).

Table 8  
% total Fatty Acids/gene

		Wild Type	<i>fad2</i>	<i>fad2</i> (LFAH12)	<i>fad2</i> (m7LFAH12)
Fatty Acid	16:0	12.57	11.40	10.93	12.14
	16:3	13.20	16.45	17.00	13.89
	18:0	1.0	0.75	0.50	1.20
	18:1	3.13	19.75	20.30	3.10
	18:2	14.33	3.95	3.70	13.09
	18:3	47.37	38.25	39.77	47.37

5

To evaluate the effect of the seven mutations on the activity of the FAD2 gene, FAD2 and m<sub>7</sub>FAD2 were expressed in the Arabidopsis *fad2* mutant under the control of the strong seed-specific promoter from the *B. rapa* napin gene (Miguel et al., 1992). The results are shown in Table 9 and presented graphically in Figure 11. The abbreviations used in Figure 11 are:

10 ricinoleic acid (18:1-OH), densipolic acid (18:2-OH) and lesquerolic acid (20:1-OH).

As expected from previous studies (Broun et al., 1998), none of the 15 transgenic lines expressing the FAD2 gene accumulated detectable hydroxy fatty acids, although the ratio of linoleate to oleate accumulation was increased an average of 10-fold as compared to untransformed controls. In the transgenic lines expressing m<sub>7</sub>FAD2, the amount of hydroxylated fatty acids, which included ricinoleic, densipolic and lesquerolic acids, comprised up to 9.4% of total seed fatty acids. The ratio of seed linoleate to oleate contents was increased an average of 6.4-fold (results not presented), which indicated that m<sub>7</sub>FAD2 exhibited significant desaturase activity, albeit lower than in the seeds of plants transformed with the wild type FAD2 gene. The high levels of hydroxy fatty acid accumulation observed in transgenic plants expressing m<sub>7</sub>FAD2 indicated that the modified desaturase had comparable levels of hydroxylase activity, in the *in planta* assay, to the native *Lesquerella* hydroxylase enzyme. However, the seven amino acid substitutions did not completely eliminate the desaturase activity of the enzyme.

25

Table 9  
% Total fatty acid/Fatty Acid

T.L.*		20:1-OH	18:2-OH	18:1-OH
	1	2.70	3.40	0.70
	2	3.50	2.40	0.95
	3	4.90	3.00	1.30
	4	4.75	3.20	1.45
	5	1.72	1.82	2.27
	6	2.98	2.39	1.55
	7	2.76	3.86	1.88
	8	3.14	4.50	1.18

\* Transgenic Line

Two approaches were used to determine whether any single amino acid residue of the seven had a major effect on the ratio of hydroxylase to desaturase activities. First, each of the seven FAD2-equivalent residues were individually introduced into the LFAH12 enzyme. None of the enzymes containing single amino acid substitutions had activities that differed significantly from the wild type hydroxylase enzyme when expressed in yeast. We also constructed seven modified LFAH12 genes containing all combinations of six desaturase-equivalent residues. The seven constructs were introduced into yeast cells, and the accumulation in these cells of ricinoleic and polyunsaturated fatty acids was measured. The results are shown in Table 10 and are shown graphically in Figure 12. Seven derivatives of the m<sub>7</sub>LFAH12 gene containing all combinations of six out of seven substitutions were introduced into yeast cells and the fatty acid composition of five independent cultures was measured. The "X" designation refers to the unmodified amino acid (i.e., enzyme XI325M contains all of the seven substitutions *except* I325M). Each of the seven lines exhibited a ratio of diunsaturated/hydroxylated fatty acids that was closer to the ratio produced by the m<sub>7</sub>FAH12 enzyme than by FAH12. Thus, for the *Lesquerella* hydroxylase, and presumably also for the *Arabidopsis* desaturase, as few as six residues principally determine the ratio of the functional outcome in terms of desaturation or hydroxylation of the enzyme. All lines showed somewhat reduced levels of desaturase activity, with the largest reductions of ~40% seen in F218Y and G105A. Therefore, we made a construct in which both these changes were combined (xF218Y/G105A). This construct exhibited similar activity to the individual F218Y and G105A mutants suggesting that their effects are redundant and that the observed changes in activity result from interactions of more than two of the seven residues. Considered together, these results indicate that no single amino acid position plays an essential role in catalytic outcome.

Rather, changes in activity result from a combined effect of several amino acid positions which have partially overlapping effects.

Table 10

% Total Fatty Acids/Fatty Acid

A.A.S.		18:2-OH	18:2	16:2
	X1325M	0.33	6.17	2.69
	XA323S	0.43	5.28	2.76
	XV296A	0.39	4.75	2.12
	XF218Y	0.94	4.22	1.84
	XN149T	0.42	4.87	1.85
	XG105A	0.63	3.89	1.65
	XV63A	0.47	5.73	2.31
	M7LFAH12	0.39	6.98	3.08
	LFAH12	1.52	0.65	0.74

5 \*Amino Acid Substitutions

Because four of the seven amino acids are adjacent to histidine residues that have been identified as essential to catalysis, we hypothesized that these four residues may be of greatest importance to the outcome of the reaction. A modified FAD2 enzyme, designated m<sub>4</sub>FAD2, was constructed in which these four amino acids were replaced by their equivalents from the Lesquerella hydroxylase: A104G, T148N, S322A, M324I. Expression of m<sub>4</sub>FAD2 in seeds of wild type Arabidopsis resulted in the accumulation of average levels of hydroxy fatty acids that were similar to those obtained with m<sub>7</sub>FAD2 (Fig. 11). Thus, only four changes are required to convert a strict desaturase to an enzyme which retains some desaturase activity but is also an efficient hydroxylase.

Biochemical and structural similarities between the desaturase and hydroxylase in addition to recent kinetic isotope experiments, suggest that there is an initial oxidation event at C-12 for both enzymes (Buist et al., 1998). We envision that since no specific single amino acid change is required, and in view of the substantial effect of the four residues that about the active site histidines, that the differences between desaturase and hydroxylase outcome is influenced by the geometry of the active site. The differences likely reflect changes in the relative positioning of the substrate with respect to an activated oxygen species, such that the conformation of the m<sub>4</sub>(or m<sub>7</sub>)FAD2, or wild type LFAH12 favors oxygen transfer rather than a second C-H bond cleavage

at C-13. This mode of evolving new catalytic activity departs from the accepted paradigm in which the evolution of new activities "involves the incorporation of new catalytic groups into the active site" (Babbitt et al., 1997).

Previous studies have shown how site specific mutagenesis can alter the specificity of enzymes, both for substrates and in terms of regiospecificity (Yuan et al., 1995; Sloane et al., 1991; and Cahoon et al., 1997). The functional outcome of an enzymatic reaction has also been altered from oxidase to oxygenase for the F208Y mutant of ribonucleotide reductase, but this was capable only of single turnover resulting in the formation of dopa-208. In contrast, the experiments described here demonstrate that a desaturase can be engineered to perform efficient hydroxylation by as few as four amino acid changes. And, conversely for a hydroxylase, the ratio of desaturation to hydroxylation can be greatly changed in favor of desaturation by changing as few as six residues. The resulting enzymes are catalytically active *in vivo* and their expression in transgenic Arabidopsis results in the accumulation of substantial levels of modified fatty acids.

The results presented here provide an insight into catalytic flexibility of diiron-containing enzymes. In addition to desaturases and hydroxylases, Stymne and collaborators have recently discovered that acetylenic and epoxy fatty acids are produced by desaturation and epoxidation of double bonds by enzymes that are structurally similar to the enzymes described here (Lee et al. 1998). Thus, it appears that variations of the same catalytic center can catalyze the formation of at least four different functional groups. Since various combinations of these four functional groups define most of the chemical complexity found among the hundreds of different fatty acids that occur in higher plants, it is now apparent that most of the chemical complexity of plant fatty acids can be accounted for by divergence of a small number of desaturases. Extrapolating from the results described here, it also seems very likely that a small number of amino acid substitutions will account for the functional divergence of desaturases, hydroxylases, epoxigenases, and acetylenic-bond forming enzymes.

Although the present invention has been described in detail with reference to its presently preferred embodiments, it will be understood by those of ordinary skill in the art that various modifications and improvements to the present invention are believed to be apparent to one skilled in the art. The embodiments were chosen and described in order to explain the principles of the invention and its practical application to thereby enable others skilled in the art to best utilize the invention in various embodiments and with various modifications as are suited to the particular use contemplated. It is intended that the scope of the invention be defined by the claims appended hereto.

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We Claim:

1. A mutant fatty acyl desaturase which has fatty acyl hydroxylase activity.
2. A modified oleate desaturase in which at least two amino acid substitutions has been made to a native oleate desaturase at an amino acid position selected from the group consisting of 69, 111, 155, 226, 304, 331, and 333 as numbered in Figure 1.
3. A modified oleate desaturase in which at least four amino acid substitutions has been made to a native oleate desaturase at an amino acid position selected from the group consisting of 69, 111, 155, 226, 304, 331, and 333 as numbered in Figure 1.
4. A modified oleate desaturase in which at least six amino acid substitutions has been made to a native oleate desaturase at an amino acid position selected from the group consisting of 69, 111, 155, 226, 304, 331, and 333 as numbered in Figure 1.
5. A modified oleate desaturase, which has been aligned for maximal amino acid sequence similarity with FAD2 oleate desaturase, in which the amino acid sequence is numbered to correspond to the numbering of the FAD2 oleate desaturase, and in which the following amino acid substitutions have been made A63V, A104G, T148N, Y217F, A295V, S322A, and M324I.
6. A modified fatty acyl desaturase in which at least the active site of a native desaturase has been mutated such that an enzymatic activity of the native desaturase has been altered but specificity for fatty acyl substrate is retained.
7. A transgenic plant containing a modified desaturase gene that has been modified so as to catalyze hydroxylation of a fatty acyl substrate of the non-modified desaturase gene.
8. A transgenic plant containing a modified oleate desaturase gene of any one of claims 2-5 that has been modified so as to catalyze hydroxylation of oleate.
9. A transgenic plant containing a gene encoding the modified desaturase of any one

of claims 1-6.

10. Oil or other fatty acyl compounds produced by a modified or mutant desaturase.
11. A method of modifying a fatty acyl desaturase to a fatty acyl hydroxylase consisting of identifying and changing amino acid residues that are conserved in functionally equivalent desaturase enzymes from various plant species but that are not identical in fatty acyl hydroxylases that exhibit significant overall sequence similarity to the fatty acyl desaturases, and which catalyze hydroxylation at one of the carbon residues on the fatty acyl substrate that is desaturated by the corresponding desaturase; said modifications being made by changing the amino acid residue so that it is identical or functionally equivalent to the amino acid residue found in the naturally occurring hydroxylase.
12. A mutant fatty acyl hydroxylase which has fatty acyl desaturase activity.
13. A modified oleate hydroxylase in which at least two amino acid substitutions has been made to a native oleate hydroxylase at an amino acid position selected from the group consisting of 69, 111, 155, 226, 304, 331, and 333 as numbered in Figure 1.
14. A modified oleate hydroxylase in which at least four amino acid substitutions has been made to a native oleate hydroxylase at an amino acid position selected from the group consisting of 69, 111, 155, 226, 304, 331, and 333 as numbered in Figure 1.
15. A modified oleate hydroxylase in which at least six amino acid substitutions has been made to a native oleate hydroxylase at an amino acid position selected from the group consisting of 69, 111, 155, 226, 304, 331, and 333 as numbered in Figure 1.
16. A modified oleate hydroxylase, which has been aligned for maximal amino acid sequence similarity with FAD2 oleate hydroxylase, in which the amino acid sequence is numbered to correspond to the numbering of the FAD2 oleate hydroxylase, and in which the following amino acid substitutions have been made V63A, G105A, N149T, F218Y, V296A, A323S, and I325M.

17. A modified fatty acyl hydroxylase in which at least the active site of a native hydroxylase has been mutated such that an enzymatic activity of the native hydroxylase has been altered but specificity for fatty acyl substrate is retained.
18. A transgenic plant containing a modified hydroxylase gene that has been modified so as to catalyze desaturation of a fatty acyl substrate of the non-modified hydroxylase gene.
19. A transgenic plant containing a modified oleate hydroxylase gene of any one of claims 13-16 that has been modified so as to catalyze desaturation of oleate.
20. A transgenic plant containing a gene encoding the modified hydroxylase of any one of claims 12-17.
21. Oil or other fatty acyl compounds produced by a modified or mutant hydroxylase.
22. A method of modifying a fatty acyl hydroxylase to a fatty acyl desaturase consisting of identifying and changing amino acid residues that are conserved in functionally equivalent desaturase enzymes from various plant species but that are not identical in fatty acyl hydroxylases that exhibit significant overall sequence similarity to the fatty acyl desaturases, and which catalyze hydroxylation at one of the carbon residues on the fatty acyl substrate that is desaturated by the corresponding desaturase; said modifications being made by changing the amino acid residue so that it is identical or functionally equivalent to the amino acid residue found in the naturally occurring desaturase.
23. A method for altering fatty acid-modifying enzymes such as desaturases, hydroxylases, epoxidases and acetylene-forming enzymes so that the product or products of the reaction catalyzed by the modified enzyme more closely resemble those produced by a different functional class of enzymes than the unmodified enzyme comprising:
- identifying a number of amino acid sequences for each of two classes of functionally distinguishable but structurally related enzymes,
  - aligning the sequences for maximal sequence identity or similarity,
  - identifying those critical amino acid residues which are identical in all members of one functional class of enzymes but differ in the other class of enzymes,

d) altering the gene or genes encoding one class of enzymes so that the critical amino acid residues of the modified enzyme are changed to more closely resemble those found at the corresponding positions in the other class of enzymes, and

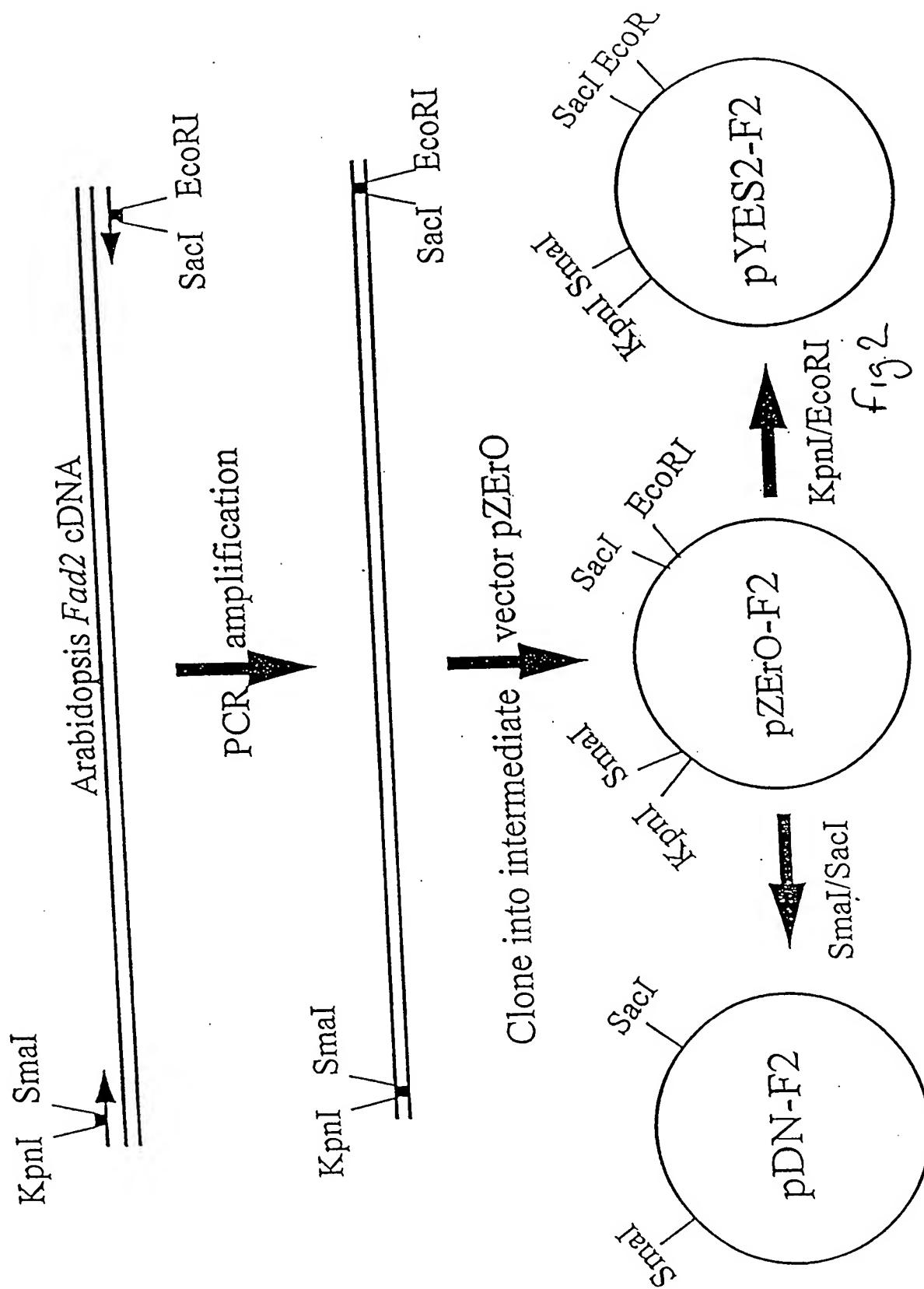
e) obtaining expression of the modified gene or genes in a host organism that is capable of transcribing and translating the gene to produce the modified enzymes of interest.

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	10	20	30	40	50	
LFFAH12	1 MGAGGRIM--	--VTPSSKKS	--ETEALKRG	PCEKPPFTVK	DLKKAIPQHC	50
FAH12	1 MGGGGRMSTV	ITSNNSEKKG	--GSSHLKRA	PHTKPPFTLG	DLKKAIPPHC	50
ATFAD2	1 MGAGGRMP--	--VPTSSKKS	--ETDITKRV	PCEKPPFSVG	DLKKAIPPHC	50
GMFAD2-1	1 MGLA-KETTM	GGRGRVAKVE	VQGGKPLSRV	PNTKPPFTVG	QLKKAIPPHC	50
GMFAD2-2	1 MGAGGR----	TDVPPANRKS	--EVDPLKRV	PFEKPPFSLF	QIKKAIPPHC	50
ZMFAD2	1 MGAGGRMTEK	EREKQEQLAR	ATGGAAMQRS	PVEKPPFTLG	QIKKAIPPHC	50
	60	70	80	90	100	
LFFAH12	51 FKRSIPRSFS	YLLTDITLVS	CFYVATNYF	SLLPQPLSTY	LAWPLYWVCQ	100
FAH12	51 FERSFVRSFS	YVAYDVCLSF	LFYSIATNFF	PYISSPLS-Y	VAWLVIWLFQ	100
ATFAD2	51 FKRSIPRSFS	YLISDIIAS	CFYVATNYF	SLLPQPLS-Y	LAWPLYWACQ	100
GMFAD2-1	51 FQSLTTSFS	YVVDLSFAF	IFY-IATTFY	HLLPQPFS-L	IAPPIYWVLQ	100
GMFAD2-2	51 FQSVLSFS	YVVDLTIAF	CLYVATHYF	HLLPGPLS-F	RGMAIYWAVQ	100
ZMFAD2	51 FERSVLKFS	YVVDLVIAA	ALLYFALAI	PALPSPLR-Y	AAWPLYWIAQ	100
	110	120	130	140	150	
LFFAH12	101 GCVLTGIWVI	GHECGHHAES	DYQWDDTVG	FIFHSFLLVP	YFSWKYSHRR	150
FAH12	101 GCILTGLWVI	GHECGHHAES	EYQLADDIVG	LIVHSALLVP	YFSWKYSHRR	150
ATFAD2	101 GCVLTGIWVI	AHECGHHAES	DYQWDDTVG	LIFHSFLLVP	YFSWKYSHRR	150
GMFAD2-1	101 GCLLTGVWVI	AHECGHHAES	KYQWDDVVG	LTLHSTLLVP	YFSWKYSHRR	150
GMFAD2-2	101 GCILTGVWVI	AHECGHHAES	DYQLDDIVG	LILHSALLVP	YFSWKYSHRR	150
ZMFAD2	101 G-----	-----AFS	DYSLDDVVG	LVLHSSLMVP	YFSWKYSHRR	150
	160	170	180	190	200	
LFFAH12	151 HHSNNGSLEK	DEVFVPPKKA	AVKWYVKYL-	NNPLGRILVL	TVQFILGWPL	200
FAH12	151 HHSNIGSLER	DEVFVPKSKS	KISWYSKYS-	NNPPGRVLT	AATLLIGWPL	200
ATFAD2	151 HHSNTGSLER	DEVFVPKQKS	AIKWYGYKL-	NNPLGRIMML	TVQFVLGWPL	200
GMFAD2-1	151 HHSNTGSLDR	DEVFVPKPKS	KVAFWSKYL-	NNPLGRAVSL	LVTLTIGWEM	200
GMFAD2-2	151 HHSNTGSLER	DEVFVPKQKS	CIKWYSKYL-	NNPPGRVLT	AVTLTLGWPL	200
ZMFAD2	151 HHSNTGSLER	DEVFVPKCKE	ALPWYTPYVY	NNPVGRVWHI	VVQLTLGWPL	200
	210	220	230	240	250	
LFFAH12	201 YLAFNVSGRP	YDG-FASHFF	PHAPIFKDRE	RLQIYISDAG	ILAVCYGLYR	250
FAH12	201 YLAFNVSGRP	YDR-FACHYD	PYGPIFSERE	RLQIYIADLG	IFATTFVLYQ	250
ATFAD2	201 YLAFNVSGRP	YDG-FACHFF	PNAPIYNDRE	RLQIYISDAG	ILAVCFGLYR	250
GMFAD2-1	201 YLAFNVSGRP	YDS-FASHYH	PYAPIYSNRE	RLLIYVSIVA	LFSVTYSLYR	250
GMFAD2-2	201 YLALNVSGRP	YDR-FACHYD	PYGPIYSNRE	RLQIYISDAG	VLAVVYGLFR	250
ZMFAD2	201 YLATNASGRP	YPR-FACHFD	PYGPIYNDRE	RAQIFVSDAG	VVAVAFGLYK	250
	260	270	280	290	300	
LFFAH12	251 YAASQGLTAM	ICVYGVPLLI	VNFFLVLTFT	LQHTHPSLPH	YDSTEWELIR	300
FAH12	251 ATMAKGLAWV	MRIYGVPLLI	VNCFVLMITY	LQHTHPAIPR	YGSSEWDWLR	300
ATFAD2	251 YAAAQGMASM	ICLYGVPLLI	VNAFLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
GMFAD2-1	251 VATLKGLVWL	LCVYGVPLLI	VNGFLVTITY	LQHTHFALPH	YDSSEWDWLR	300
GMFAD2-2	251 LAMAKGLAWV	VCVYGVPLLV	VNGFLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
ZMFAD2	251 LAAAFGVWVW	VRVYAVPLLI	VNAWLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
	310	320	330	340	350	
LFFAH12	301 GALVTVDROY	GILNKVFHNI	TDTHVAHHLF	ATIPHYNAME	ATEAIKPILG	350
FAH12	301 GAMVTVDROY	GVLNKVFHNI	ADTHVAHHLF	ATVPHYNAME	ATKAIKPILG	350
ATFAD2	301 GALATVDROY	GILNKVFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIKPILG	350
GMFAD2-1	301 GALATMDROY	GILNKVFHNI	TDTHVAHHLF	STMPHYNAME	ATNAIKPILG	350
GMFAD2-2	301 GALATVDROY	GILNKVFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIKPILG	350
ZMFAD2	301 GALATMDROY	GILNRVFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIRPILG	350
	360	370	380	390	400	
LFFAH12	351 DYYHFDGTPW	YVAMYREAKE	CLYVEPDTER	GKKGVYVYNN	K-L.....	400
FAH12	351 EYYRYDGTFF	YKALWREAKE	CLFVEPDDEGA	PTQGVFWYRN	KY-.....	400
ATFAD2	351 DYYQFDGTPW	YVAMYREAKE	CIYVEPDREG	DKKGVYVYNN	K-L.....	400
GMFAD2-1	351 EYYQFDDTFF	YKALWREAKE	CLYVEPDDEGT	SEKGVYVYRN	KY-.....	400
GMFAD2-2	351 EYYRFDDETF	VKAMWREAKE	CIYVEPDQST	ESKGVFWYNN	KL-.....	400
ZMFAD2	351 DYYHFDPTPV	AKATWREAKE	CIYVEPE---	DRKGVFWYNN	KF*.....	400

Fig 1

# General strategy for site directed mutagenesis of Arabidopsis *Fad2*



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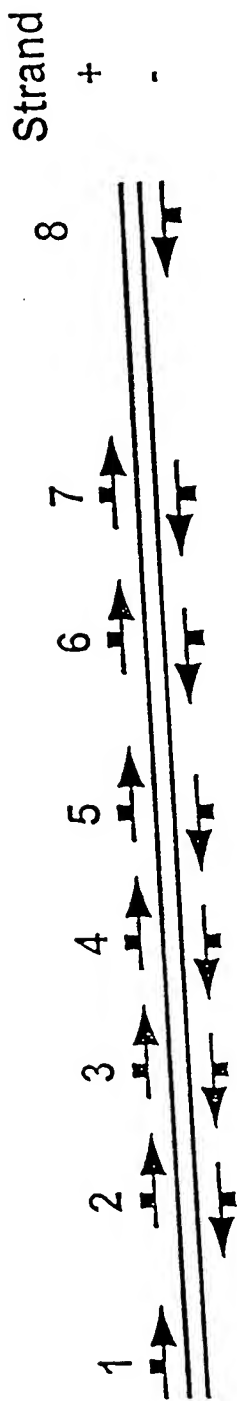
1	Met	Gly	Ala	Gly	Gly	Arg	Met	Pro	Val	Pro	Thr	Ser	Ser	Lys	Lys	Ser	16
1	ATG	GGT	GCA	GGT	GGA	AGA	ATG	CCG	GTT	CCT	ACT	TCT	TCC	AAG	AAA	TCG	48
17	Glu	Thr	Asp	Thr	Thr	Lys	Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Ser	32
49	GAA	ACC	GAC	ACC	ACA	AAG	CGT	GTG	CCG	TGC	GAG	AAA	CCG	CCT	TTC	TCG	96
33	Val	Gly	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser	48
97	GTG	GGA	GAT	CTG	AAG	AAA	GCA	ATC	CCG	CCG	CAT	TGT	TTC	AAA	CGC	TCA	144
49	Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Ser	Asp	Ile	Ile	Ile	Ala	Ser	64
145	ATC	CCT	CGC	TCT	TTC	TCC	TAC	CTT	ATC	AGT	GAC	ATC	ATT	ATA	GCC	TCA	192
65	Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro	80
193	TGC	TTC	TAC	TAC	GTC	GCC	ACC	AAT	TAC	TTC	TCT	CTC	CTC	CCT	CAG	CCT	240
81	Leu	Ser	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val	96
241	CTC	TCT	TAC	TTG	GCT	TGG	CCA	CTC	TAT	TGG	GCC	TGT	CAA	GCC	TGT	GTC	288
97	Leu	Thr	Gly	Ile	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe	112
289	CTA	ACT	GGT	ATC	TGG	GTC	ATA	GCC	CAC	GAA	TGC	GGT	CAC	CAC	GCA	TTC	336
113	Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser	128
337	AGC	GAC	TAC	CAA	TGG	CTG	GAT	GAC	ACA	GTT	GGT	CTT	ATC	TTC	CAT	TCC	384
129	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His	144
385	TTC	CTC	CTC	GTC	CCT	TAC	TTC	TCC	TGG	AAG	TAT	AGT	CAT	CGC	CGT	CAC	432
145	His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys	160
433	CAT	TCC	AAC	ACT	GGA	TCC	CTC	GAA	AGA	GAT	GAA	GTA	TTT	GTC	CCA	AAG	480
161	Gln	Lys	Ser	Ala	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu	176
481	CAG	AAA	TCA	GCA	ATC	AAG	TGG	TAC	GGG	AAA	TAC	CTC	AAC	AAC	CCT	CTT	528
177	Gly	Arg	Ile	Met	Met	Leu	Thr	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro	Leu	192
529	GGA	CGC	ATC	ATG	ATG	TTA	ACC	GTC	CAG	TTT	GTC	CTC	GGG	TGG	CCC	TTG	576
193	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala	Cys	208
577	TAC	TTA	GCC	TTT	AAC	GTC	TCT	GGC	AGA	CCG	TAT	GAC	GGG	TTC	GCT	TGC	624
209	His	Phe	Phe	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	Gln	224
625	CAT	TTC	TTC	CCC	AAC	GCT	CCC	ATC	TAC	AAT	GAC	CGA	GAA	CGC	CTC	CAG	672
225	Ile	Tyr	Leu	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Phe	Gly	Leu	Tyr	240
673	ATA	TAC	CTC	TCT	GAT	GCG	GGT	ATT	CTA	GCC	GTC	TGT	TTT	GGT	CTT	TAC	720
241	Arg	Tyr	Ala	Ala	Ala	Gln	Gly	Met	Ala	Ser	Met	Ile	Cys	Leu	Tyr	Gly	256
721	CGT	TAC	GCT	GCT	GCA	CAA	GGG	ATG	GCC	TCG	ATG	ATC	TGC	CTC	TAC	GGA	768
257	Val	Pro	Leu	Leu	Ile	Val	Asn	Ala	Phe	Leu	Val	Leu	Ile	Thr	Tyr	Leu	272
769	GTA	CCG	CTT	CTG	ATA	GTG	AAT	GCG	TTC	CTC	GTC	TTG	ATC	ACT	TAC	TTG	816
273	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp	288
817	CAG	CAC	ACT	CAT	CCC	TCG	TTG	CCT	CAC	TAC	GAT	TCA	TCA	GAG	TGG	GAC	864
289	Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	Leu	304
865	TGG	CTC	AGG	GGA	GCT	TTG	GCT	ACC	GTA	GAC	AGA	GAC	TAC	GGA	ATC	TTG	912
305	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His	Leu	320
913	AAC	AAG	GTG	TTC	CAC	AAC	ATT	ACA	GAC	ACA	CAC	GTG	GCT	CAT	CAC	CTG	960
321	Phe	Ser	Thr	Met	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Lys	Ala	Ile	336
961	TTC	TCG	ACA	ATG	CCG	CAT	TAT	AAC	GCA	ATG	GAA	GCT	ACA	AAG	GCG	ATA	1008

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337	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Trp	Tyr	352
1009	AAG	CCA	ATT	CTG	GGA	GAC	TAT	TAC	CAG	TTC	GAT	GGA	ACA	CCG	TGG	TAT	1056
353	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro	Asp	368
1057	GTA	GCG	ATG	TAT	AGG	GAG	GCA	AAG	GAG	TGT	ATC	TAT	GTA	GAA	CCG	GAC	1104
369	Arg	Glu	Gly	Asp	Lys	Lys	Gly	Val	Tyr	Trp	Tyr	Asn	Asn	Lys	Leu	***	384
1105	AGG	GAA	GGT	GAC	AAG	AAA	GGT	GTG	TAC	TGG	TAC	AAC	AAT	AAG	TTA	TGA	1152

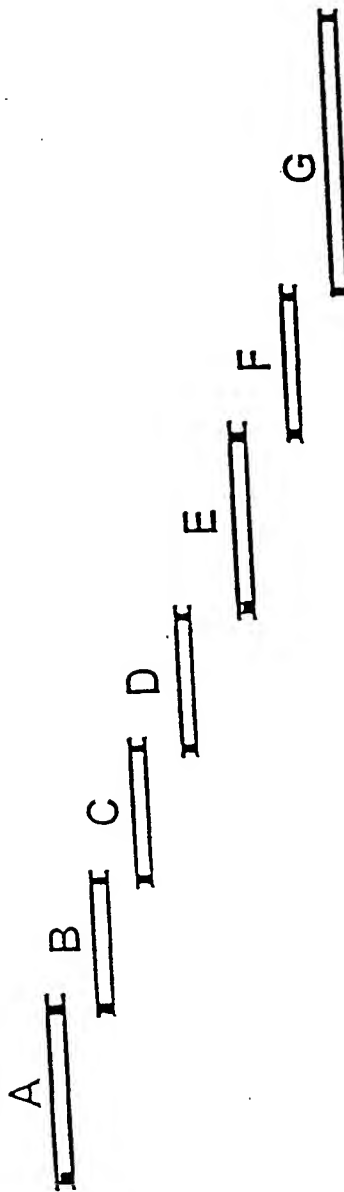
Fig 3 continued



■ Desired mutations

Product of first round PCRs using *Fad2* cDNA as template

Oligos  
+,-  
1,2  
2,3  
3,4  
4,5  
5,6  
6,7  
7,8



Product of second round overlap-extension PCR using fragments A-H as template

1,8



Fig4

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MFAD2                   10                   20                   30                   40                   50                   60  
ATGGGTGCAGGTGGAAGAATGCCGGTTCCTACTTCTTCCAAGAAATCGGAAACCGACACC  
FAD2                   ATGGGTGCAGGTGGAAGAATGCCGGTTCCTACTTCTTCCAAGAAATCGGAAACCGACACC

MFAD2                   70                   80                   90                   100                   110                   120  
ACAAAGCGTGTGCCGTGCGAGAAACCGCCTTTCTCGGTGGGAGATCTGAAGAAAGCAATC  
FAD2                   ACAAAGCGTGTGCCGTGCGAGAAACCGCCTTTCTCGGTGGGAGATCTGAAGAAAGCAATC

MFAD2                   130                   140                   150                   160                   170                   180  
CCGCCGCATTGTTTCAAACGCTCAATCCCTCGCTCTTTCTCCTACCTTATCAGTGACATC  
FAD2                   CCGCCGCATTGTTTCAAACGCTCAATCCCTCGCTCTTTCTCCTACCTTATCAGTGACATC

MFAD2                   190                   200                   210                   220                   230                   240  
ATTATAGTCTCATGCTTCTACTACGTCGCCACCAATTACTTCTCTCTCCTCCCTCAGCCT  
FAD2                   ATTATAGCCTCATGCTTCTACTACGTCGCCACCAATTACTTCTCTCTCCTCCCTCAGCCT

MFAD2                   250                   260                   270                   280                   290                   300  
CTCTCTTACTTGGCTTGGCCACTCTATTGGGCCTGTCAAGGCTGTGTCTTAACCTGGTATC  
FAD2                   CTCTCTTACTTGGCTTGGCCACTCTATTGGGCCTGTCAAGGCTGTGTCTTAACCTGGTATC

MFAD2                   310                   320                   330                   340                   350                   360  
TGGGTCATAGGCCACGAATGCCGTACACGCTTACGCGACTACCAATGGCTGGATGAC  
FAD2                   TGGGTCATAGGCCACGAATGCCGTACACGCTTACGCGACTACCAATGGCTGGATGAC

MFAD2                   370                   380                   390                   400                   410                   420  
ACAGTTGGTCTTATCTTCCATTCCCTCCTCGTCCCTTACTTCTCCTGGAAGTATAGT  
FAD2                   ACAGTTGGTCTTATCTTCCATTCCCTCCTCGTCCCTTACTTCTCCTGGAAGTATAGT

MFAD2                   430                   440                   450                   460                   470                   480  
CATCGCCGTACCATTTCCAACAATGGATCCCTCGAAAGAGATGAAGTATTTGTCCCAAAG  
FAD2                   CATCGCCGTACCATTTCCAACAATGGATCCCTCGAAAGAGATGAAGTATTTGTCCCAAAG

MFAD2                   490                   500                   510                   520                   530                   540  
CAGAAATCAGCAATCAAGTGGTACGGGAAATACCTCAACAACCCTCTTGGACGCATCATG  
FAD2                   CAGAAATCAGCAATCAAGTGGTACGGGAAATACCTCAACAACCCTCTTGGACGCATCATG

MFAD2                   550                   560                   570                   580                   590                   600  
ATGTTAACCGTCCAGTTTGTCTCGGGTGGCCCTTGTACTTAGCCTTTAACGTCTCTGGC  
FAD2                   ATGTTAACCGTCCAGTTTGTCTCGGGTGGCCCTTGTACTTAGCCTTTAACGTCTCTGGC

MFAD2                   610                   620                   630                   640                   650                   660  
AGACCGTATGACGGGTTCGCTTGCCATTTCTTCCCCAACGCTCCCATCTTCAATGACCGA  
FAD2                   AGACCGTATGACGGGTTCGCTTGCCATTTCTTCCCCAACGCTCCCATCTTCAATGACCGA

MFAD2                   670                   680                   690                   700                   710                   720  
GAACGCCTCCAGATATACCTCTCTGATGCGGGTATTCTAGCCGTCTGTTTTGGTCTTTAC  
FAD2                   GAACGCCTCCAGATATACCTCTCTGATGCGGGTATTCTAGCCGTCTGTTTTGGTCTTTAC

MFAD2                   730                   740                   750                   760                   770                   780  
CGTTACGCTGCTGCACAAGGGATGGCCTCGATGATCTGCCTCTACGGAGTACCGCTTCTG  
FAD2                   CGTTACGCTGCTGCACAAGGGATGGCCTCGATGATCTGCCTCTACGGAGTACCGCTTCTG

fig 5a

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```

      790      800      810      820      830      840
MFAD2  ATAGTGAATGCGTTCCTCGTCTTGATCACTTACTTGCAGCACACTCATCCCTCGTTGCCT
      .....
FAD2   ATAGTGAATGCGTTCCTCGTCTTGATCACTTACTTGCAGCACACTCATCCCTCGTTGCCT

      850      860      870      880      890      900
MFAD2  CACTACGATTCATCAGAGTGGGACTGGCTCAGGGGAGCTTTGGTTACCGTAGACAGAGAC
      .....
FAD2   CACTACGATTCATCAGAGTGGGACTGGCTCAGGGGAGCTTTGGCTACCGTAGACAGAGAC

      910      920      930      940      950      960
MFAD2  TACGGAATCTTGAACAAGGTGTTCCACAACATTACAGACACACACGTGGCTCATCACCTG
      .....
FAD2   TACGGAATCTTGAACAAGGTGTTCCACAACATTACAGACACACACGTGGCTCATCACCTG

      970      980      990      1000      1010      1020
MFAD2  TTCGCGACAATACCGCATTATAACGCAATGGAAGCTACAAAGGCGATAAAGCCAATTCTG
      .....
FAD2   TTCTCGACAATGCCGCATTATAACGCAATGGAAGCTACAAAGGCGATAAAGCCAATTCTG

      1030      1040      1050      1060      1070      1080
MFAD2  GGAGACTATTACCAGTTCGATGGAACACCGTGGTATGTAGCGATGTATAGGGAGGCAAAG
      .....
FAD2   GGAGACTATTACCAGTTCGATGGAACACCGTGGTATGTAGCGATGTATAGGGAGGCAAAG

      1090      1100      1110      1120      1130      1140
MFAD2  GAGTGTATCTATGTAGAACCGGACAGGGAAGGTGACAAGAAAGGTGTGTACTGGTACAAC
      .....
FAD2   GAGTGTATCTATGTAGAACCGGACAGGGAAGGTGACAAGAAAGGTGTGTACTGGTACAAC

      1150
MFAD2  AATAAGTTATGA
      .....
FAD2   AATAAGTTATGA
```

fig 5b

1 10 20 30 40 50 60  
FAD2 MGAGGRMPVPTSSKKSETDTTKRVPCEKPPFSVGD LKKAIPPHCFKRSIPRSFSYLISDI  
MFAD2 MGAGGRMPVPTSSKKSETDTTKRVPCEKPPFSVGD LKKAIPPHCFKRSIPRSFSYLISDI  
1 10 20 30 40 50 60

61 70 80 90 100 110 120  
FAD2 IIASCFYVATNYFSLLPQPLSYLAWPLYWACQGCVL TGIWVIAHECGHHAFSDYQWLDD  
MFAD2 IIIVSCFYVATNYFSLLPQPLSYLAWPLYWACQGCVL TGIWVIGHECGHHAFSDYQWLDD  
61 70 80 90 100 110 120

121 130 140 150 160 170 180  
FAD2 TVGLIFHSFLLVPYFSWKYSHRRHHSNTGSLERDE VFPKQKSAIKWYGKYLNNPLGRIM  
MFAD2 TVGLIFHSFLLVPYFSWKYSHRRHHSNNGSLERDE VFPKQKSAIKWYGKYLNNPLGRIM  
121 130 140 150 160 170 180

181 190 200 210 220 230 240  
FAD2 MLTVQFVLGWPLYLAFNVSGRPYDGFACHFFPNAPI YNDRERLQIYLS DAGILAVCFGLY  
MFAD2 MLTVQFVLGWPLYLAFNVSGRPYDGFACHFFPNAPI FNDRERLQIYLS DAGILAVCFGLY  
181 190 200 210 220 230 240

241 250 260 270 280 290 300  
FAD2 RYAAAQGMASMICLYGVPLLI VNAFLVLITYLQHTHPSLPHYDSSEWDWLRGALATVD RD  
MFAD2 RYAAAQGMASMICLYGVPLLI VNAFLVLITYLQHTHPSLPHYDSSEWDWLRGALATVD RD  
241 250 260 270 280 290 300

301 310 320 330 340 350 360  
FAD2 YGILNKVFHNITDTHVAHHLFSTMPHYNAMEATKA IKPILGDYYQFDGTPWYVAMYREAK  
MFAD2 YGILNKVFHNITDTHVAHHLFATIPHYNAMEATKA IKPILGDYYQFDGTPWYVAMYREAK  
301 310 320 330 340 350 360

361 370 380  
FAD2 ECIYVEPDREGDKKGVYWYNNKL\*  
MFAD2 ECIYVEPDREGDKKGVYWYNNKL\*  
361 370 380

Fig 6

Fig 6

	10	20	30	40	50	60
LFAH12	ATGGGTGCTGGTGGAAGAATAATGGTTACCCCCCTCTTCCAAGAAATCAGAAACTGAAGCC					
MLFAH12	ATGGGTGCTGGTGGAAGAATAATGGTTACCCCCCTCTTCCAAGAAATCAGAAACTGAAGCC					
	70	80	90	100	110	120
LFAH12	CTAAACCGTGACCATGTGAGAAACCACCATTACTGTTAAAGATCTGAAGAAAGCAATC					
MLFAH12	CTAAACCGTGACCATGTGAGAAACCACCATTACTGTTAAAGATCTGAAGAAAGCAATC					
	130	140	150	160	170	180
LFAH12	CCACAGCATTGTTTTCAACGCTCTATCCCTCGTTCTTTCTCTACCTTCTCACAGATATC					
MLFAH12	CCACAGCATTGTTTTCAACGCTCTATCCCTCGTTCTTTCTCTACCTTCTCACAGATATC					
	190	200	210	220	230	240
LFAH12	ACTTTAGTTTCTTGCTTCTACTACGTTGCCACAAATTACTTCTCTTCTCCCTCAGCCT					
MLFAH12	ACTTTAGCTTCTTGCTTCTACTACGTTGCCACAAATTACTTCTCTTCTCCCTCAGCCT					
	250	260	270	280	290	300
LFAH12	CTCTCTACTTACCTAGCTTGGCCTCTCTATTGGGTATGTCAAGGCTGTGTCTTAACCGGT					
MLFAH12	CTCTCTACTTACCTAGCTTGGCCTCTCTATTGGGTATGTCAAGGCTGTGTCTTAACCGGT					
	310	320	330	340	350	360
LFAH12	ATCTGGGTCATTGGCCATGAATGTGGTCACCATGCATTCAAGTACTATCAATGGGTAGAT					
MLFAH12	ATCTGGGTCATTGGCCATGAATGTGGTCACCATGCATTCAAGTACTATCAATGGGTAGAT					
	370	380	390	400	410	420
LFAH12	GACACTGTTGGTTTTATCTTCCATTCCCTTCCTTCTCGTTCCCTTACTTCTCTCTGGAAGTAC					
MLFAH12	GACACTGTTGGTTTTATCTTCCATTCCCTTCCTTCTCGTTCCCTTACTTCTCTCTGGAAGTAC					
	430	440	450	460	470	480
LFAH12	AGTCATCGCCGTCACCATTTCCAACAATGGATCCCTAGAAAAAGATGAAGTCTTTGTCCCA					
MLFAH12	AGTCATCGCCGTCACCATTTCCAACAATGGATCCCTAGAAAAAGATGAAGTCTTTGTCCCA					
	490	500	510	520	530	540
LFAH12	CCTAAGAAAGCTGCAGTCAAATGGTATGTTAAATACCTCAACAACCTCTTGGACGCATT					
MLFAH12	CCTAAGAAAGCTGCAGTCAAATGGTATGTTAAATACCTCAACAACCTCTTGGACGCATT					
	550	560	570	580	590	600
LFAH12	TTGGTGTTAACAGTTCAGTTTATCCTCGGGTGGCCTTTGTATCTAGCCTTTAATGTATCA					
MLFAH12	TTGGTGTTAACAGTTCAGTTTATCCTCGGGTGGCCTTTGTATCTAGCCTTTAATGTATCA					
	610	620	630	640	650	660
LFAH12	GGTAGACCTTATGATGGTTTCGCTTCACATTCTTCCCTCATGCACCTATCTTAAAGGAC					
MLFAH12	GGTAGACCTTATGATGGTTTCGCTTCACATTCTTCCCTCATGCACCTATCTTAAAGGAC					
	670	680	690	700	710	720
LFAH12	CGTGAACGTCTCCAGATATACATCTCAGATGCTGGTATTCTAGCTGTCTGTTATGGTCTT					
MLFAH12	CGTGAACGTCTCCAGATATACATCTCAGATGCTGGTATTCTAGCTGTCTGTTATGGTCTT					
	730	740	750	760	770	780
LFAH12	TACCGTTACGCTGCTTCACAAGGATTGACTGCTATGATCTGCGTCTATGGAGTACCGCTT					
MLFAH12	TACCGTTACGCTGCTTCACAAGGATTGACTGCTATGATCTGCGTCTATGGAGTACCGCTT					

Fig 7

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	790	800	810	820	830	840
LFAH12	TGGATTGTAAACTTCTTCCTTGTCCTTGGTCACCTTCTTGACGACACACTCATCCTTCATTA					
MLFAH12	TGGATTGTAAACTTCTTCCTTGTCCTTGGTCACCTTCTTGACGACACACTCATCCTTCATTA					
	850	860	870	880	890	900
LFAH12	CCTCACTATGATTCAACCGAATGGGAATGGATTAGAGGAGCTTTGGTTACGGTAGACAGA					
MLFAH12	CCTCACTATGATTCAACCGAATGGGAATGGATTAGAGGAGCTTTGGCTACGGTAGACAGA					
	910	920	930	940	950	960
LFAH12	GACTATGGAATCTTGAACAAGGTGTTCCATAACATAACAGACACACATGTGGCTCATCAT					
MLFAH12	GACTATGGAATCTTGAACAAGGTGTTCCATAACATAACAGACACACATGTGGCTCATCAT					
	970	980	990	1000	1010	1020
LFAH12	CTCTTTTGCAACTATACCGCATTATAACGCAATGGAAGCTACAGAGGCGATAAAGCCAATA					
MLFAH12	CTCTTTTCAACTATGCCGCATTATAACGCAATGGAAGCTACAGAGGCGATAAAGCCAATA					
	1030	1040	1050	1060	1070	1080
LFAH12	CTTGGTGATTACTACCATTTTCGATGGGACACCTTGGTATGTGGCTATGTATAGGGAAGCA					
MLFAH12	CTTGGTGATTACTACCATTTTCGATGGGACACCTTGGTATGTGGCTATGTATAGGGAAGCA					
	1090	1100	1110	1120	1130	1140
LFAH12	AAGGAGTGTCTTTATGTTGAACCGGATACCGAACGTGGGAAGGAAGGTGTTTACTATTAC					
MLFAH12	AAGGAGTGTCTTTATGTTGAACCGGATACCGAACGTGGGAAGGAAGGTGTTTACTATTAC					
	1150					
LFAH12	AACAATAAGTTATGA					
MLFAH12	AACAATAAGTTATGA					

*Fig 7 continued*

		10	20	30	40	50	
LFAH12	MGAGGRIMVTPSSKKKSETEALKRGPCEKPPFTVKDLKKAIPQHCFQRSIPRSFSYLLTDI	60					
	.....						
MFAH12	MGAGGRIMVTPSSKKKSETEALKRGPCEKPPFTVKDLKKAIPQHCFQRSIPRSFSYLLTDI	60					
	.....						
		10	20	30	40	50	
		70	80	90	100	110	
LFAH12	TLVSCFYVATNYFSLLPQPLSTYLAWPLYWVCQGCVLTTGIWVIGHECGHHAFSDYQWVD	120					
	.....						
MFAH12	TLVSCFYVATNYFSLLPQPLSTYLAWPLYWVCQGCVLTTGIWVIAHECGHHAFSDYQWVD	120					
	.....						
		70	80	90	100	110	
		130	140	150	160	170	
LFAH12	DTVGFIHFSFLLVPYFSWKYSHRRHHSNNGSLEKDEVFVPPKKA AVKWYVKYLN NPLGRI	180					
	.....						
MFAH12	DTVGFIHFSFLLVPYFSWKYSHRRHHSNTGSLEKDEVFVPPKKA AVKWYVKYLN NPLGRI	180					
	.....						
		130	140	150	160	170	
		200	210	220	230	240	
LFAH12	LVLTVQFILGWPLYLAFNVSGRPYDGFASHFFPHAPIFKDRERLQIYISDAGILAVCYGL	250					
	.....						
MFAH12	LVLTVQFILGWPLYLAFNVSGRPYDGFASHFFPHAPIYKDRERLQIYISDAGILAVCYGL	250					
	.....						
		200	210	220	230	240	
		260	270	280	290	300	
LFAH12	YRYAASQGLTAMICVYGVP LWIVNFFLVLVTF LQHTHPSLPHYDSTEW EWIRGALVTVD R	310					
	.....						
MFAH12	YRYAASQGLTAMICVYGVP LWIVNFFLVLVTF LQHTHPSLPHYDSTEW EWIRGALATVD R	310					
	.....						
		260	270	280	290	300	
		320	330	340	350	360	
LFAH12	DYGILNKVFHNITDTHVAHHLFATIPHYNAMEATEAIKPILGDYYHFDGTPWYVAMYREA	370					
	.....						
MFAH12	DYGILNKVFHNITDTHVAHHLFSTMPHYNAMEATEAIKPILGDYYHFDGTPWYVAMYREA	370					
	.....						
		320	330	340	350	360	
		380	390				
LFAH12	KECLYVEPDTERGKEGVYYNNKL						
	.....						
MFAH12	KECLYVEPDTERGKEGVYYNNKL						
	.....						
		380	390				

Figure 8

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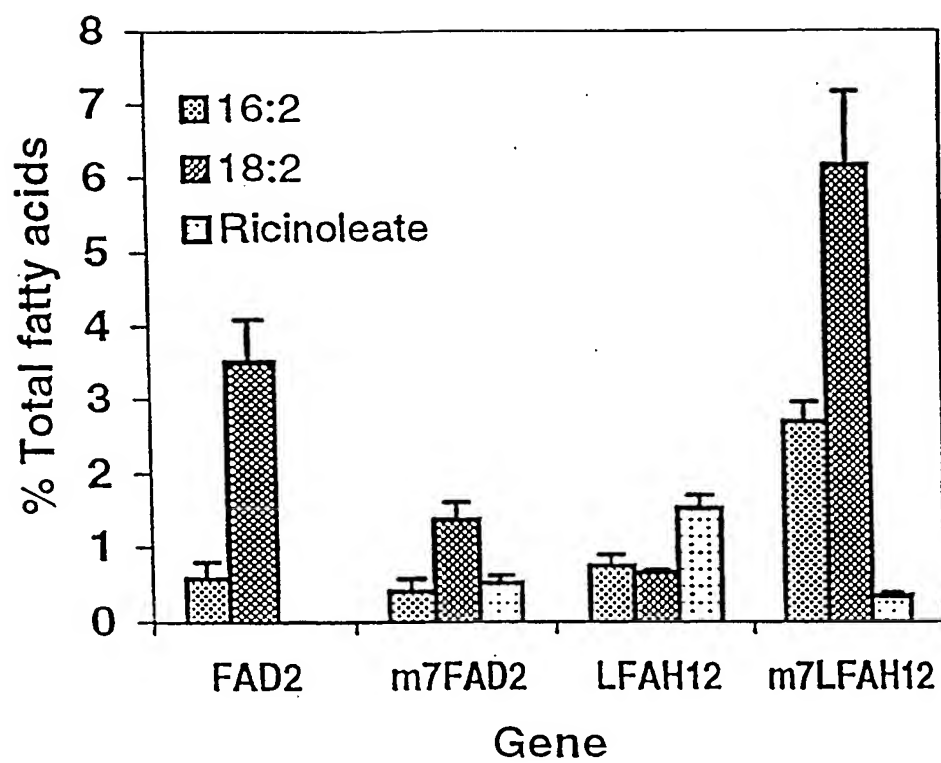


FIGURE 9

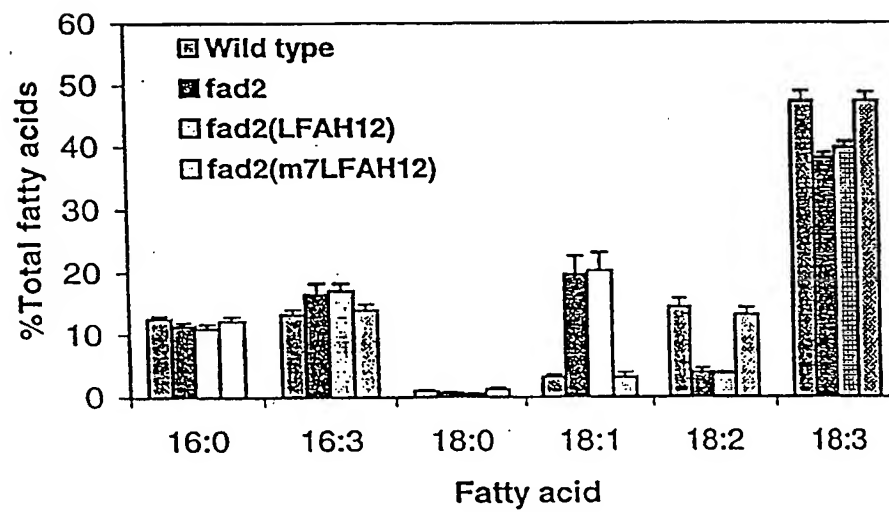


FIGURE 10

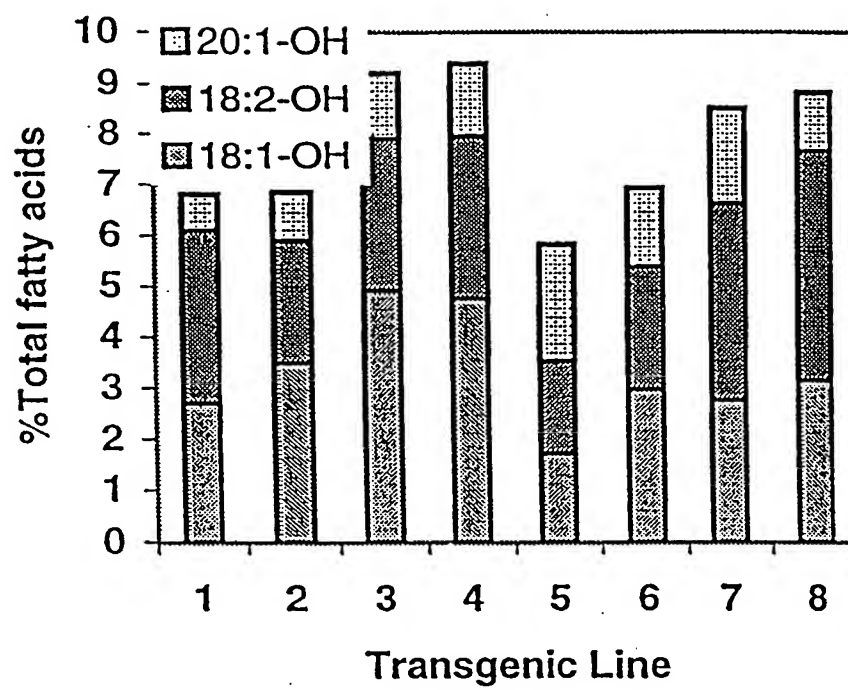


FIGURE 11

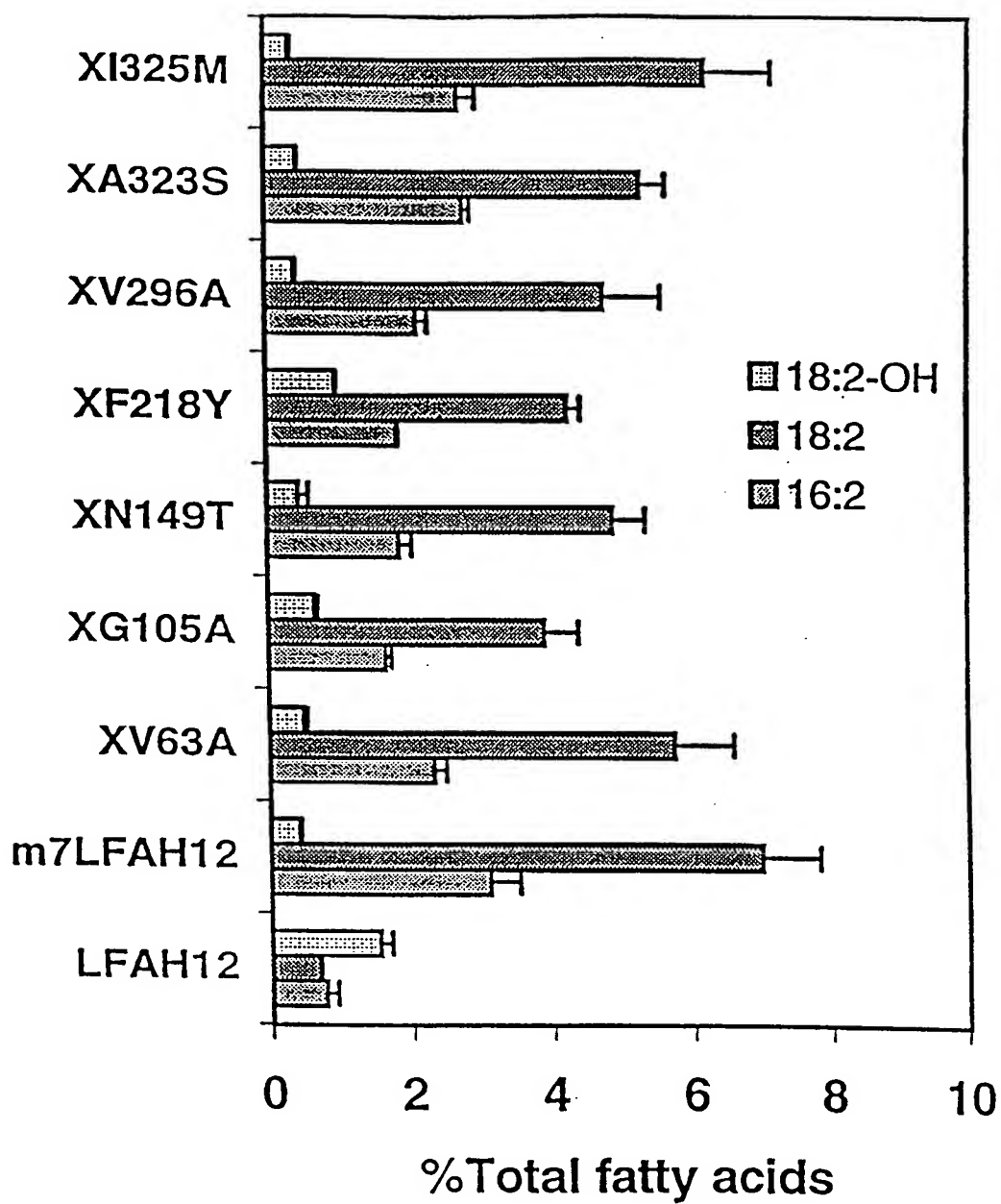


FIGURE 12

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Pierre Broun  
John Shanklin  
Chris Somerville
- (ii) TITLE OF INVENTION: INTERCONVERSION OF  
DESATURASES AND HYDROXYLASES
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: PILLSBURY MADISON & SUTRO
  - (B) STREET: 1100 NEW YORK AVENUE, N.W.
  - (C) CITY: WASHINGTON
  - (D) STATE: D.C.
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 20005-3918
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: 3.5 inch, 1.44 MB storage
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: MS-DOS/PC-DOS
  - (D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1152 nucleotides
  - (B) TYPE: nucleotide
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGGTGCAG	GTGGAAGAAT	GCCGGTTCCT	ACTTCTTCCA	40
AGAAATCGGA	AACCGACACC	ACAAAGCGTG	TGCCGTGCGA	80
GAAACCGCCT	TTCTCGGTGG	GAGATCTGAA	GAAAGCAATC	120
CCGCCGCATT	GTTTCAAACG	CTCAATCCCT	CGCTCTTTCT	160
CCTACCTTAT	CAGTGACATC	ATTATAGTCT	CATGCTTCTA	200
CTACGTCGCC	ACCAATTACT	TCTCTCTCCT	CCCTCAGCCT	240
CTCTCTTACT	TGGCTTGGCC	ACTCTATTGG	GCCTGTCAAG	280
GCTGTGTCCT	AACTGGTATC	TGGGTCATAG	GCCACGAATG	320
CGGTCACCAC	GCATTCAGCG	ACTACCAATG	GCTGGATGAC	360
ACAGTTGGTC	TTATCTTCCA	TTCCTTCCTC	CTCGTCCCTT	400

ACTTCTCCTG	GAAGTATAGT	CATCGCCGTC	ACCATTCCAA	440
CAATGGATCC	CTCGAAAGAG	ATGAAGTATT	TGTCCCAAAG	480
CAGAAATCAG	CAATCAAGTG	GTACGGGAAA	TACCTCAACA	520
ACCCTCTTGG	ACGCATCATG	ATGTTAACCG	TCCAGTTTGT	560
CCTCGGGTGG	CCCTTGTA	TAGCCTTTAA	CGTCTCTGGC	600
AGACCGTATG	ACGGGTTCGC	TTGCCATTTT	TTCCCCAACG	640
CTCCCATCTT	CAATGACCGA	GAACGCCTCC	AGATATACCT	680
CTCTGATGCG	GGTATTCTAG	CCGTCTGTTT	TGGTCTTTAC	720
CGTTACGCTG	CTGCACAAGG	GATGGCCTCG	ATGATCTGCC	760
TCTACGGAGT	ACCGCTTCTG	ATAGTGAATG	CGTTCCTCGT	800
CTTGATCACT	TACTTGCAGC	ACACTCATCC	CTCGTTGCCT	840
CACTACGATT	CATCAGAGTG	GGACTGGCTC	AGGGGAGCTT	880
TGGTTACCGT	AGACAGAGAC	TACGGAATCT	TGAACAAGGT	920
GTTCCACAAC	ATTACAGACA	CACACGTGGC	TCATCACCTG	960
TTCCGCACAA	TACCGCATT	TAACGCAATG	GAAGCTACAA	1000
AGGCGATAAA	GCCAATTCTG	GGAGACTATT	ACCAGTTCGA	1040
TGGAACACCG	TGGTATGTAG	CGATGTATAG	GGAGGCAAAG	1080
GAGTGTATCT	ATGTAGAACC	GGACAGGGAA	GGTGACAAGA	1120
AAGGTGTGTA	CTGGTACAAC	AATAAGTTAT	GA	1152

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Ala	Gly	Gly	Arg	Met	Pro	Val	Pro	5	10
Thr	Ser	Ser	Lys	Lys	Ser	Glu	Thr	Asp	Thr	15	20
Thr	Lys	Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	25	30
Phe	Ser	Val	Gly	Asp	Leu	Lys	Lys	Ala	Ile	35	40
Pro	Pro	His	Cys	Phe	Lys	Arg	Ser	Ile	Pro	45	50
Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Ser	Asp	Ile	55	60
Ile	Ile	Val	Ser	Cys	Phe	Tyr	Tyr	Val	Ala	65	70
Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro		

75	80
Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp	
85	90
Ala Cys Gln Gly Cys Val Leu Thr Gly Ile	
95	100
Trp Val Ile Gly His Glu Cys Gly His His	
105	110
Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp	
115	120
Thr Val Gly Leu Ile Phe His Ser Phe Leu	
125	130
Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser	
135	140
His Arg Arg His His Ser Asn Asn Gly Ser	
145	150
Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
155	160
Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys	
165	170
Tyr Leu Asn Asn Pro Leu Gly Arg Ile Met	
175	180
Met Leu Thr Val Gln Phe Val Leu Gly Trp	
185	190
Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly	
195	200
Arg Pro Tyr Asp Gly Phe Ala Cys His Phe	
205	210
Phe Pro Asn Ala Pro Ile Phe Asn Asp Arg	
215	220
Glu Arg Leu Gln Ile Tyr Leu Ser Asp Ala	
225	230
Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr	
235	240
Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser	
245	250

Met Ile Cys Leu Tyr Gly Val Pro Leu Leu  
255 260

Ile Val Asn Ala Phe Leu Val Leu Ile Thr  
265 270

Tyr Leu Gln His Thr His Pro Ser Leu Pro  
275 280

His Tyr Asp Ser Ser Glu Trp Asp Trp Leu  
285 290

Arg Gly Ala Leu Val Thr Val Asp Arg Asp  
295 300

Tyr Gly Ile Leu Asn Lys Val Phe His Asn  
305 310

Ile Thr Asp Thr His Val Ala His His Leu  
315 320

Phe Ala Thr Ile Pro His Tyr Asn Ala Met  
325 330

Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu  
335 340

Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro  
345 350

Trp Tyr Val Ala Met Tyr Arg Glu Ala Lys  
355 360

Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu  
365 370

Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn  
375 380

Asn Lys Leu

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1155 nucleotides
  - (B) TYPE: nucleotide
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGGTGCTG GTGGAAGAAT AATGGTTACC CCCTCTTCCA	40
AGAAATCAGA AACTGAAGCC CTAAAACGTG GACCATGTGA	80

GAAACCACCA	TTTACTGTTA	AAGATCTGAA	GAAAGCAATC	120
CCACAGCATT	GTTTTCAACG	CTCTATCCCT	CGTTCTTTCT	160
CCTACCTTCT	CACAGATATC	ACTTTAGCTT	CTTGCTTCTA	200
CTACGTTGCC	ACAAATTACT	TCTCTCTTCT	CCCTCAGCCT	240
CTCTCTACTT	ACCTAGCTTG	GCCTCTCTAT	TGGGTATGTC	280
AAGGCTGTGT	CTTAACCGGT	ATCTGGGTCA	TGCCCATGA	320
ATGTGGTCAC	CATGCATTCA	GTGACTATCA	ATGGGTAGAT	360
GACACTGTTG	GTTTTATCTT	CCATTCCTTC	CTTCTCGTTC	400
CTTACTTCTC	CTGGAAGTAC	AGTCATCGCC	GTCACCATTC	440
CAACACTGGA	TCCCTAGAAA	AAGATGAAGT	CTTTGTCCCA	480
CCTAAGAAAG	CTGCAGTCAA	ATGGTATGTT	AAATACCTCA	520
ACAACCCTCT	TGGACGCATT	TTGGTGTTAA	CAGTTCAGTT	560
TATCCTCGGG	TGGCCTTTGT	ATCTAGCCTT	TAATGTATCA	600
GGTAGACCTT	ATGATGGTTT	CGCTTCACAT	TTCTTCCCTC	640
ATGCACCTAT	CTATAAGGAC	CGTGAACGTC	TCCAGATATA	680
CATCTCAGAT	GCTGGTATTC	TAGCTGTCTG	TTATGGTCTT	720
TACCGTTACG	CTGCTTCACA	AGGATTGACT	GCTATGATCT	760
GCGTCTATGG	AGTACCGCTT	TGGATTGTAA	ACTTCTTCCT	800
TGTCTTGGTC	ACTTTCTTGC	AGCACACTCA	TCCTTCATTA	840
CCTCACTATG	ATTCAACCGA	ATGGGAATGG	ATTAGAGGAG	880
CTTTGGCTAC	GGTAGACAGA	GACTATGGAA	TCTTGAACAA	920
GGTGTTCAT	AACATAACAG	ACACACATGT	GGCTCATCAT	960
CTCTTTTCAA	CTATGCCGCA	TTATAACGCA	ATGGAAGCTA	1000
CAGAGGCGAT	AAAGCCAATA	CTTGGTGATT	ACTACCATTT	1040
CGATGGGACA	CCTTGGTATG	TGGCTATGTA	TAGGGAAGCA	1080
AAGGAGTGTC	TTTATGTTGA	ACCGGATACC	GAACGTGGGA	1120
AGGAAGGTGT	TTACTATTAC	AACAATAAGT	TATGA	1155

## (2) INFORMATION FOR SEQ ID NO:4

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ala Gly Gly Arg Ile Met Val Thr	
	5 10
Pro Ser Ser Lys Lys Ser Glu Thr Glu Ala	
	15 20
Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro	
	25 30
Phe Thr Val Lys Asp Leu Lys Lys Ala Ile	
	35 40
Pro Gln His Cys Phe Gln Arg Ser Ile Pro	
	45 50

Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile  
 55 60  
 Thr Leu Ala Ser Cys Phe Tyr Tyr Val Ala  
 65 70  
 Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
 75 80  
 Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr  
 85 90  
 Trp Val Cys Gln Gly Cys Val Leu Thr Gly  
 95 100  
 Ile Trp Val Ile Ala His Glu Cys Gly His  
 105 110  
 His Ala Phe Ser Asp Tyr Gln Trp Val Asp  
 115 120  
 Asp Thr Val Gly Phe Ile Phe His Ser Phe  
 125 130  
 Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr  
 135 140  
 Ser His Arg Arg His His Ser Asn Thr Gly  
 145 150  
 Ser Leu Glu Lys Asp Glu Val Phe Val Pro  
 155 160  
 Pro Lys Lys Ala Ala Val Lys Trp Tyr Val  
 165 170  
 Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile  
 175 180  
 Leu Val Leu Thr Val Gln Phe Ile Leu Gly  
 185 190  
 Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser  
 195 200  
 Gly Arg Pro Tyr Asp Gly Phe Ala Ser His  
 205 210  
 Phe Phe Pro His Ala Pro Ile Tyr Lys Asp  
 215 220  
 Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp  
 225 230

Ala Gly Ile Leu	Ala Val Cys Tyr Gly Leu	
235		240
Tyr Arg Tyr Ala	Ala Ser Gln Gly Leu Thr	
245		250
Ala Met Ile Cys	Val Tyr Gly Val Pro Leu	
255		260
Trp Ile Val Asn	Phe Phe Leu Val Leu Val	
265		270
Thr Phe Leu Gln	His Thr His Pro Ser Leu	
275		280
Pro His Tyr Asp	Ser Thr Glu Trp Glu Trp	
285		290
Ile Arg Gly Ala	Leu Ala Thr Val Asp Arg	
295		300
Asp Tyr Gly Ile	Leu Asn Lys Val Phe His	
305		310
Asn Ile Thr Asp	Thr His Val Ala His His	
315		320
Leu Phe Ser Thr	Met Pro His Tyr Asn Ala	
325		330
Met Glu Ala Thr	Glu Ala Ile Lys Pro Ile	
335		340
Leu Gly Asp Tyr	Tyr His Phe Asp Gly Thr	
345		350
Pro Trp Tyr Val	Ala Met Tyr Arg Glu Ala	
355		360
Lys Glu Cys Leu	Tyr Val Glu Pro Asp Thr	
365		370
Glu Arg Gly Lys	Glu Gly Val Tyr Tyr Tyr	
375		380
Asn Asn Lys Leu		

Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	235	240
Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr	245	250
Ala Met Ile Cys Val Tyr Gly Val Pro Leu	255	260
Trp Ile Val Asn Phe Phe Leu Val Leu Val	265	270
Thr Phe Leu Gln His Thr His Pro Ser Leu	275	280
Pro His Tyr Asp Ser Thr Glu Trp Glu Trp	285	290
Ile Arg Gly Ala Leu Ala Thr Val Asp Arg	295	300
Asp Tyr Gly Ile Leu Asn Lys Val Phe His	305	310
Asn Ile Thr Asp Thr His Val Ala His His	315	320
Leu Phe Ser Thr Met Pro His Tyr Asn Ala	325	330
Met Glu Ala Thr Glu Ala Ile Lys Pro Ile	335	340
Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr	345	350
Pro Trp Tyr Val Ala Met Tyr Arg Glu Ala	355	360
Lys Glu Cys Leu Tyr Val Glu Pro Asp Thr	365	370
Glu Arg Gly Lys Glu Gly Val Tyr Tyr Tyr	375	380
Asn Asn Lys Leu		